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2147	2156
2148	2157

val ser ser ala arg phe arg lys val asp val asp
glu tyr asp glu asn lys phe val asp glu glu asp
gly gly asp gly gln ala gly pro asp glu gly glu
val asp ser cys leu arg gln gly asn met thr ala
ala leu gln ala ala leu lys asn pro pro ile asn
thr **arg** ser gln ala val lys asp arg ala gly ser
ile val leu lys val leu ile ser phe lys ala **gly**
asp ile glu lys ala val gln ser leu asp **arg** asn
gly val asp leu leu met lys tyr ile tyr lys gly
phe glu ser pro ser asp asn ser ser ala **val** leu
leu gln trp his glu lys ala leu ala ala gly gly
val gly ser ile val arg val leu thr ala arg lys
thr val

Fig. 2A (1/3)

ggctctgtgtg tgcgtgcgtg cgagtgcgtg agtgtgtgca tttttttttt tctctttttt	60
ttctctctct tttttttttt ttgcaaaga aacagcagcg ccgcccgcgc tccgcgcagg	120
cgctgcgccc cccggggggg ggaggcggag gaggcgggca gcggcggagg gaggggagcc	180
ggggaggggg ggcgcgcgcg gggagggagg cagcgcgcac ggtgcagccg ggcggggcgg	240
gagge atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc	290
Met Ala Gly Pro Pro Ala Leu Pro Pro Glu Thr Ala Ala Ala	
1 5 10 15	
gcc acc acg gcc gcg gcc gcc gcc tgc tgc tcc gcc gct tcc ccg cac	338
Ala Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His	
20 25 30	
tac caa gag tgg att ctg gac acc atc gac tgc ctg cgc tgc cgc aag	386
Tyr Gln Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys	
35 40 45	
gcg cgg ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac	434
Ala Arg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His	
50 55 60	
ggc ccg gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag	482
Gly Pro Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln	
65 70 75	
cag cgc gcc gtg ctc cgg gtc agc tac aag ggg agc atc tgc tac cgc	530
Gln Arg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg	
80 85 90 95	
aac gcg gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc	578
Asn Ala Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala	
100 105 110	
ccg ccg cgc gcc ccc cgc ggg ggc ccc gcc gcc gcc gcc gcc gcg ccg ccg	626
Pro Pro Arg Ala Pro Arg Gly Gly Pro Ala Ala Ala Ala Ala Pro Pro	
115 120 125	
ccc acg ccc gcc ccg ccg ccg ccg ccc gcg ccc gtc gcc gcc gcc gcc	674
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala	
130 135 140	
gcc ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gcc gct gcc gcc aca	722
Ala Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Ala Thr	
145 150 155	
gcg ccc ccc tgc ccc ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg	770
Ala Pro Pro Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg	
160 165 170 175	
gcc gcg ccc ctg gcc gcg ccg ccg ccc gcg ccc gcc gct ccc ccg gcg	818
Ala Ala Pro Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala	
180 185 190	

Fig. 2A (continued 2/3)

gcg gcg ccc ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gcc gcc	866
Ala Ala Pro Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Ala Ala	
195 200 205	
gtc gcc gcc cgg gag tgc ccg ctg ccg ccg ccg cca cag ccg ccg gcg	914
Val Ala Ala Arg Glu Ser Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala	
210 215 220	
ccg cca cag cag cag cag cag ccg ccg ccg cca ccg ccg ccg cag cag	962
Pro Pro Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Gln	
225 230 235	
cca cag ccg ccg ccg gag ggg ggc gcg gcg ccg gcc ggc ggc ccg gcg	1010
Pro Gln Pro Pro Pro Glu Gly Gly Ala Ala Arg Ala Gly Gly Pro Ala	
240 245 250 255	
ccg ccc gtg agc ctg ccg gaa gtc gtg cgc tac ctc ggg ggt agc agc	1058
Arg Pro Val Ser Leu Arg Glu Val Val Arg Tyr Leu Gly Gly Ser Ser	
260 265 270	
ggc gct ggc ggc cgc ctg acc cgc gcc cgc gcg cag ggt ctg ctg gaa	1106
Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg Val Gln Gly Leu Leu Glu	
275 280 285	
gag gag gcg gcg gcg ccg ggc cgc ctg gag cgc acc cgt ctc gga gcg	1154
Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu Arg Thr Arg Leu Gly Ala	
290 295 300	
ctt gcg ctg ccc cgc ggg gac agg ccc gga ccg gcg cca ccg gcc gcc	1202
Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly Arg Ala Pro Pro Ala Ala	
305 310 315	
agc gcc cgc gcg gcg ccg aac aag aga gct ggc gag gag cga gtg ctt	1250
Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala Gly Glu Glu Arg Val Leu	
320 325 330 335	
gaa aag gag gag gag gag gag gag gag gaa gac gac gag gac gac gac	1298
Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp Asp	
340 345 350	
gac gac gtc gtg tcc gag ggc tgc gag gtg ccc gag agc gat cgt ccc	1346
Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg Pro	
355 360 365	
gcg ggt gcg cag cat cac cag ctg aat ggc ggc gag cgc ggc ccg cag	1394
Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro Gln	
370 375 380	
acc gcc aag gag ccg gcc aag gag tgg tgc ctg tgt ggc ccc cac cct	1442
Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His Pro	
385 390 395	
ggc cag gag gaa ggg ccg ggg ccg gcc gcg ggc agt ggc acc cgc cag	1490
Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg Gln	
400 405 410 415	

Fig. 2A (continued 3/3)

gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct tcg	1538
Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser	
420 425 430	
acg acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg aag	1586
Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys	
435 440 445	
cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc ggg	1634
Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly	
450 455 460	
cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac gtc	1682
Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val	
465 470 475	
gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct ttc	1730
Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe	
480 485 490 495	
cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc acc	1778
Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg Thr	
500 505 510	
gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa atc	1826
Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile	
515 520 525	
tat gag cac cat atc aag gtg ctg cag cag ggt cac ttc gag gac gat	1874
Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp	
530 535 540	
gac ccg gaa ggc ttc ctg gga t gagcacagag ccgcccgcgc ccttggtccc	1926
Asp Pro Glu Gly Phe Leu Gly	
545 550	
acccccaccc cgccctggacc cattcctgcc tccatgtcac ccaaggtgtc ccagaggcca	1986
ggagctggac tgggcaggcg aggggtgcgg acctaccctg attctggtag ggggcggggc	2046
cttgctgtgc tcattgctac cccccaccc cgtgtgtgtc tctgcacctg cccccagcac	2106
acccctcccg gagcctggat gtcgcctggg actctggcct gctcattttg cccccagatc	2166
agccccctcc ctccctcctg tcccaggaca ttttttaaaa gaaaaaaagg aaaaaaaaaa	2226
attggggagg gggctgggaa ggtgcccaca gatcctcctc ggcccaaacca ggtgtttatt	2286
cctatatata tatatatatg ttttgttctg cctgtttttc gtttttttgt gcgtggcctt	2346
tcttccctcc caccaccact catggcccca gccctgctcg ccctgtcggc gggagcagct	2406
gggaatggga ggagggtggg accttgggtc tgtctccac cctctctccc gtttggttctg	2466
ttgtcgtccc agctggctgt attgcttttt aatattgcac cgaagggttg tttttttttt	2526
tttaataaaa attttaaaaa aaggaaaaaa aaaaa	2561

Fig. 3

ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu glu
glu glu glu glu asp **asp** glu **asp** **asp** asp asp **asp**
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn **gly**
gly glu arg gly pro gln **thr** ala lys glu arg **ala**
lys glu trp **ser** leu cys gly pro his **pro** gly gln
glu glu gly arg gly pro ala **ala** gly ser gly thr
arg gln val phe ser met ala ala **leu** **ser** lys glu
gly gly **ser** ala ser **ser** **thr** thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro **ala** asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

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Fig. 5 (continued)

leu ala glu arg leu lys lys leu ile glu gln tyr
glu leu arg glu glu his ile asp lys val phe lys
his lys asp leu gln gln gln leu val asp ala lys
leu gln gln ala gln glu met leu lys glu ala glu
glu arg his gln arg glu lys asp phe leu leu lys
glu ala val glu ser gln arg met cys glu leu met
lys gln gln glu thr his leu lys gln gln leu ala
leu tyr thr glu lys phe glu glu phe gln asn thr
leu ser lys ser ser glu val phe thr thr phe lys
gln glu met glu lys met thr lys lys ile lys lys
leu glu lys glu thr thr met tyr arg ser arg trp
glu ser ser asn lys ala leu leu glu met ala glu
glu lys thr leu arg asp lys glu leu glu gly leu
gln val lys ile gln arg leu glu lys leu cys arg
ala leu gln thr glu arg asn asp leu asn lys arg
val gln asp leu ser ala gly gly gln gly **pro val**
ser asp ser gly pro glu arg arg pro **glu pro ala**
thr thr ser lys glu gln gly val glu gly pro gly
ala gln **val** pro **asn** ser pro arg **ala thr asp ala**
ser cys **cys ala** gly ala pro ser thr glu ala ser
gly gln thr gly pro gln glu pro thr **thr ala thr**
ala

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Fig. 6

met ser lys asn thr val ser ser ala
arg phe arg lys val asp val asp glu tyr asp glu
asn lys phe val asp glu glu asp gly gly asp gly
gln ala gly pro asp glu gly glu val asp ser cys
leu arg gln gly asn met thr ala ala leu gln ala
ala leu lys asn pro pro ile asn thr **lys** ser gln
ala val lys asp arg ala gly ser ile val leu lys
val leu ile ser phe lys ala **asn** asp ile glu lys
ala val gln ser leu asp **lys** asn gly val asp leu
leu met lys tyr ile tyr lys gly phe glu ser pro
ser asp asn ser ser ala **met** leu leu gln trp his
glu lys ala leu ala ala gly gly val gly ser ile
val arg val leu thr ala arg lys thr val

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Fig. 7A (1/3)

atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc gcc	48
Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala Ala	
1 5 10 15	
acc acg gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac tac caa	96
Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His Tyr Gln	
20 25 30	
gag tgg atc ctg gac acc atc gac tcg ctg cgc tcg cgc aag gcg cgg	144
Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala Arg	
35 40 45	
ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac gcc ccg	192
Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro	
50 55 60	
gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag cag cgc	240
Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln Arg	
65 70 75 80	
gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc aac gcg	288
Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala	
85 90 95	
gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc ccg ccg	336
Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro	
100 105 110	
cgc gcc ccc cgc ggg gcc ccc gcc gcc gcc gcc gcc gcc gcc gcc	384
Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Ala Pro Pro	
115 120 125	
ccc acg ccc gcc ccg ccg cca ccg ccc gcg ccc gtc gcc gcc gcc gcc	432
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala	
130 135 140	
ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gcc gcc aca gcg ccc ccc	480
Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Thr Ala Pro Pro	
145 150 155 160	
tcg cct ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg gcc gcg ccc	528
Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro	
165 170 175	
ctg gcc gcg ccg ccg ccc gcg cca gcc gct ccc ccg gcg gtg gcg ccc	576
Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Val Ala Pro	
180 185 190	
ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gtc gcc gcc ccg gag	624
Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu	
195 200 205	
ccg ccg ctg ccg ccg ccg cca cag ccg ccg gcg ccg cca cag cag cag	672
Pro Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln	
210 215 220	

Fig. 7A (continued; 2/3)

cag ccg ccg ccg ccg cag cca cag ccg ccg ccg gag ggg ggc gcg gtg	720
Gln Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Glu Gly Gly Ala Val	
225 230 235 240	
cgg gcc ggc ggc gcg gcg ccg ccc gtg agc ctg ccg gaa gtc gtg cgc	768
Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg	
245 250 255	
tac ctc ggg ggc agc ggc ggc gcc ggc ggt cgc cta acc cgc ggc cgc	816
Tyr Leu Gly Gly Ser Gly Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg	
260 265 270	
gtg cag ggg ctg ctg gag gag gag gcg gcg gct cga ggc cgt ctg gag	864
Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu	
275 280 285	
cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga	912
Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly	
290 295 300	
cgg gcg ccg ccg gcc gcc agc gcc ccg cct cgc agc aag aga ggt	960
Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly	
305 310 315 320	
gga gaa gag cga gta ctt gag aaa gaa gag gaa gaa gat gat gat gaa	1008
Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu	
325 330 335	
gat gaa gat gaa gaa gat gat gtg tca gag ggc tct gaa gtg ccc gag	1056
Asp Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu	
340 345 350	
agt gac cgt cct gca ggt gcc cag cac cac cag ctt aac ggc gag ccg	1104
Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg	
355 360 365	
gga cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga	1152
Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly	
370 375 380	
ccg cac cag ggc cag gat gaa ggg ccg ggg cca gcc ccg ggc agc ggc	1200
Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly	
385 390 395 400	
acc cgc cag gtg ttc tcc atg gca gcc atg aac aag gaa ggg gga aca	1248
Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr	
405 410 415	
gct tct gtt gcc acc ggg cca gac tcc ccg tcc ccc gtg cct ttg ccc	1296
Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro	
420 425 430	
cca gcc aaa cca gcc cta cct ggg gcc gac ggg acc ccc ttt ggc tgt	1344
Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys	
435 440 445	

Variable	Mean	SD	Min	Max
Age	35.2	12.5	18	65
Gender	Male	10.5	0	20
Marital Status	Married	15.2	0	20
Education	High School	12.5	0	20
Income	\$30,000	\$15,000	\$10,000	\$50,000
Health Status	Good	10.5	0	20
Exercise Frequency	Weekly	12.5	0	20
Stress Level	Low	10.5	0	20
Sleep Quality	Good	10.5	0	20
Dietary Habits	Healthy	10.5	0	20
Work-Life Balance	Good	10.5	0	20
Family Support	High	10.5	0	20
Community Involvement	Active	10.5	0	20
Life Satisfaction	High	10.5	0	20
Overall Well-being	Good	10.5	0	20

1392
1440
1488
1536
1584
1614

Fig. 7B

glu glu arg val leu glu lys glu glu glu glu **asp**
asp asp glu asp glu **asp glu glu** asp asp val ser
glu gly ser glu val pro glu ser asp arg pro ala
gly ala gln his his gln leu asn gly glu arg gly
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**
pro cys gly pro his **gln** gly gln **asp** glu gly arg
gly pro ala **pro** gly ser gly thr arg gln val phe
ser met ala ala **met asn** lys glu gly gly **thr** ala
ser **val ala** thr gly pro asp ser pro ser pro val
pro leu pro pro gly lys pro ala leu pro gly ala
asp gly thr pro phe gly cys pro **pro** gly arg lys
glu lys pro **ser** asp pro val glu trp thr val met
asp val val glu tyr phe thr glu ala gly phe pro
glu gln ala thr ala phe gln glu gln glu ile asp
gly lys ser leu leu leu met gln arg thr asp val
leu thr gly leu ser ile arg leu gly pro ala leu
lys ile tyr glu his his ile lys val leu gln gln
gly his phe glu asp asp asp pro **asp** gly phe leu
gly

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[illegible]

atg	aag	aac	caa	gac	aaa	aag	aac	ggg	gct	gcc	aaa	caa	tcc	aat	cca	48
Met	Lys	Asn	Gln	Asp	Lys	Lys	Asn	Gly	Ala	Ala	Lys	Gln	Ser	Asn	Pro	
1				5					10					15		
aaa	agc	agc	cca	gga	caa	ccg	gaa	gca	gga	ccc	gag	gga	gcc	cag	gag	96
Lys	Ser	Ser	Pro	Gly	Gln	Pro	Glu	Ala	Gly	Pro	Glu	Gly	Ala	Gln	Glu	
			20					25					30			
cgg	ccc	agc	cag	gcg	gct	cct	gca	gta	gaa	gca	gaa	ggc	ccc	ggc	agc	144
Arg	Pro	Ser	Gln	Ala	Ala	Pro	Ala	Val	Glu	Ala	Glu	Gly	Pro	Gly	Ser	
		35					40					45				
agc	cag	gct	cct	cgg	aag	ccg	gag	ggc	gct	caa	gcc	aga	acg	gct	cag	192
Ser	Gln	Ala	Pro	Arg	Lys	Pro	Glu	Gly	Ala	Gln	Ala	Arg	Thr	Ala	Gln	
	50					55					60					
tct	ggg	gcc	ctt	cgt	gat	gtc	tct	gag	gag	ctg	agc	cgc	caa	ctg	gaa	240
Ser	Gly	Ala	Leu	Arg	Asp	Val	Ser	Glu	Glu	Leu	Ser	Arg	Gln	Leu	Glu	
65				70						75				80		
gac	ata	ctg	agc	aca	tac	tgt	gtg	gac	aat	aac	cag	ggg	ggc	ccc	ggc	288
Asp	Ile	Leu	Ser	Thr	Tyr	Cys	Val	Asp	Asn	Asn	Gln	Gly	Gly	Pro	Gly	
				85					90					95		
gag	gat	ggg	gca	cag	ggt	gag	ccg	gct	gaa	ccc	gaa	gat	gca	gag	aag	336
Glu	Asp	Gly	Ala	Gln	Gly	Glu	Pro	Ala	Glu	Pro	Glu	Asp	Ala	Glu	Lys	
			100					105					110			
tcc	cgg	acc	tat	gtg	gca	agg	aat	ggg	gag	cct	gaa	cca	act	cca	gta	384
Ser	Arg	Thr	Tyr	Val	Ala	Arg	Asn	Gly	Glu	Pro	Glu	Pro	Thr	Pro	Val	
		115					120					125				
gtc	aat	gga	gag	aag	gaa	ccc	tcc	aag	ggg	gat	cca	aac	aca	gaa	gag	432
Val	Asn	Gly	Glu	Lys	Glu	Pro	Ser	Lys	Gly	Asp	Pro	Asn	Thr	Glu	Glu	
	130					135					140					
atc	cgg	cag	agt	gac	gag	gtc	gga	gac	cga	gac	cat	cga	agg	cca	cag	480
Ile	Arg	Gln	Ser	Asp	Glu	Val	Gly	Asp	Arg	Asp	His	Arg	Arg	Pro	Gln	
145				150						155					160	
gag	aag	aaa	aaa	gcc	aag	ggt	ttg	ggt	aag	gag	atc	acg	ttg	ctg	atg	528
Glu	Lys	Lys	Lys	Ala	Lys	Gly	Leu	Gly	Lys	Glu	Ile	Thr	Leu	Leu	Met	
				165					170					175		
cag	aca	ttg	aat	act	ctg	agt	acc	cca	gag	gag	aag	ctg	gct	gct	ctg	576
Gln	Thr	Leu	Asn	Thr	Leu	Ser	Thr	Pro	Glu	Glu	Lys	Leu	Ala	Ala	Leu	
			180					185					190			
tgc	aag	aag	tat	gct	gaa	ctg	ctg	gag	gag	cac	cgg	aat	tca	cag	aag	624
Cys	Lys	Lys	Tyr	Ala	Glu	Leu	Leu	Glu	Glu	His	Arg	Asn	Ser	Gln	Lys	
		195					200					205				

Fig. 8A (continued; 2/3)

cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag aag	672
Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys	
210 215 220	
gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc aag	720
Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys	
225 230 235 240	
ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc aag	768
Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys	
245 250 255	
gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag gag	816
Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys Glu	
260 265 270	
gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag atg	864
Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met	
275 280 285	
gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg gag	912
Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu	
290 295 300	
ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc gag	960
Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu	
305 310 315 320	
gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag ctg	1008
Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln Leu	
325 330 335	
gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca gaa	1056
Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala Glu	
340 345 350	
gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta gag	1104
Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu	
355 360 365	
tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg aag	1152
Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys	
370 375 380	
caa cag ott gcc cta tac aca gag aag ttt gag gag ttc cag aac aca	1200
Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr	
385 390 395 400	
ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg gaa	1248
Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu	
405 410 415	

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	15.5	10.5	5	35
Health	1.5	0.5	1	2
Stress	2.5	1.5	1	5
Life satisfaction	4.5	1.5	1	7
Work satisfaction	3.5	1.5	1	6
Family satisfaction	4.5	1.5	1	7
Community satisfaction	3.5	1.5	1	6
Overall life satisfaction	4.5	1.5	1	7
Depression	1.5	0.5	1	2
Anxiety	1.5	0.5	1	2
Stress management	2.5	1.5	1	5
Life goals	3.5	1.5	1	6
Work goals	3.5	1.5	1	6
Family goals	3.5	1.5	1	6
Community goals	3.5	1.5	1	6
Overall life goals	3.5	1.5	1	6
Depression management	2.5	1.5	1	5
Anxiety management	2.5	1.5	1	5
Stress management strategies	2.5	1.5	1	5
Life goals achievement	3.5	1.5	1	6
Work goals achievement	3.5	1.5	1	6
Family goals achievement	3.5	1.5	1	6
Community goals achievement	3.5	1.5	1	6
Overall life goals achievement	3.5	1.5	1	6
Depression management strategies	2.5	1.5	1	5
Anxiety management strategies	2.5	1.5	1	5
Stress management strategies	2.5	1.5	1	5
Life goals achievement strategies	3.5	1.5	1	6
Work goals achievement strategies	3.5	1.5	1	6
Family goals achievement strategies	3.5	1.5	1	6
Community goals achievement strategies	3.5	1.5	1	6
Overall life goals achievement strategies	3.5	1.5	1	6

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	15.5	10.5	5	35
Health	1.5	0.5	1	2
Stress	2.5	1.5	1	5
Life satisfaction	4.5	1.5	1	7
Work satisfaction	3.5	1.5	1	6
Family satisfaction	4.5	1.5	1	7
Community satisfaction	3.5	1.5	1	6
Overall life satisfaction	4.5	1.5	1	7
Depression	1.5	0.5	1	2
Anxiety	1.5	0.5	1	2
Stress management	2.5	1.5	1	5
Life goals	3.5	1.5	1	6
Work goals	3.5	1.5	1	6
Family goals	3.5	1.5	1	6
Community goals	3.5	1.5	1	6
Overall life goals	3.5	1.5	1	6
Depression management	2.5	1.5	1	5
Anxiety management	2.5	1.5	1	5
Stress management strategies	2.5	1.5	1	5
Life goals achievement	3.5	1.5	1	6
Work goals achievement	3.5	1.5	1	6
Family goals achievement	3.5	1.5	1	6
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Depression management strategies	2.5	1.5	1	5
Anxiety management strategies	2.5	1.5	1	5
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Work goals achievement strategies	3.5	1.5	1	6
Family goals achievement strategies	3.5	1.5	1	6
Community goals achievement strategies	3.5	1.5	1	6
Overall life goals achievement strategies	3.5	1.5	1	6

Fig. 8 B

lys ser ser pro gly gln pro glu ala gly pro glu gly ala
gln glu arg pro ser gln ala ala pro ala val glu ala glu gly
pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala
arg thr ala gln ser gly ala leu arg asp val ser glu glu leu
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn
asn gln gly gly pro gly glu asp gly ala gln gly glu pro ala
glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn
gly glu pro glu pro thr pro val val tyr gly glu lys glu pro
ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu
val gly asp arg asp his arg arg pro gln glu lys lys lys ala
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys
tyr ala glu leu leu glu glu his arg asn ser gln lys gln met
lys leu leu gln lys lys gln ser gln leu val gln glu lys asp
his leu arg gly glu his ser lys ala val leu ala arg ser lys
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg
lys glu val thr ser his phe gln val thr leu asn asp ile gln
leu gln met glu gln his asn glu arg asn ser lys leu arg gln
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln
tyr glu leu arg glu glu his ile asp lys val phe lys his lys
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln
glu met leu lys glu ala glu glu arg his gln arg glu lys asp
phe leu leu lys glu ala val glu ser gln arg met cys glu leu
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

00976740-104004

Fig. 8 B(continued)

glu val phe thr thr phe lys gln glu met glu lys met thr lys
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys
thr val arg asp lys glu leu glu gly leu gln val lys ile gln
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp
leu asn lys arg val gln asp leu ser ala gly gly gln gly ser
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala
gln ala pro ser ser pro arg val thr glu ala pro cys tyr pro
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu
pro thr ser ala arg ala ***

00076740-101303

Fig. 10

1	AAG	CCT	CGC	AGC	GGT	CGG	GGC	GGC	GCC	GCG	GAG	GCT
37	CGA	GGG	CGG	CGG	GCG	GCG	GCG	ATG	TCG	AAG	AAC	ACG
								met	ser	lys	asn	thr
73	GTG	TCG	TCG	GCG	CGG	TTC	CGG	AAG	GTG	GAC	GTG	GAT
	val	ser	ser	ala	arg	phe	arg	lys	val	asp	val	asp
109	GAG	TAC	GAC	GAG	AAC	AAG	TTC	GTG	GAC	GAG	GAA	GAC
	glu	tyr	asp	glu	asn	lys	phe	val	asp	glu	glu	asp
145	GGC	GGC	GAC	GGC	CAG	GCG	GGG	CCG	GAC	GAG	GGC	GAG
	gly	gly	asp	gly	gln	ala	gly	pro	asp	glu	gly	glu
181	GTG	GAC	TCG	TGC	CTG	CGG	CAA	GGG	AAC	ATG	ACA	GCC
	val	asp	ser	cys	leu	arg	gln	gly	asn	met	thr	ala
217	GCC	CTG	CAG	GCG	GCG	CTG	AAG	AAC	CCT	CCC	ATC	AAC
	ala	leu	gln	ala	ala	leu	lys	asn	pro	pro	ile	asn
253	ACC	AGG	AGC	CAG	GCG	GTG	AAG	GAC	CGG	GCA	GGC	AGC
	thr	arg	ser	gln	ala	val	lys	asp	arg	ala	gly	ser
289	ATC	GTG	CTG	AAG	GTG	CTC	ATC	TCC	TTC	AAG	GCC	GGC
	ile	val	leu	lys	val	leu	ile	ser	phe	lys	ala	gly
325	GAC	ATA	GAA	AAG	GCC	GTG	CAG	TCC	CTG	GAC	AGG	AAC
	asp	ile	glu	lys	ala	val	gln	ser	leu	asp	arg	asn
361	GGC	GTG	GAC	CTG	CTC	ATG	AAG	TAC	ATC	TAC	AAG	GGC
	gly	val	asp	leu	leu	met	lys	tyr	ile	tyr	lys	gly
397	TTC	GAG	AGC	CCC	TCC	GAC	AAC	AGC	AGC	GCC	GTG	CTC
	phe	glu	ser	pro	ser	asp	asn	ser	ser	ala	val	leu
433	CTG	CAG	TGG	CAC	GAG	AAG	GCG	CTG	GCT	GCA	GGA	GGA
	leu	gln	trp	his	glu	lys	ala	leu	ala	ala	gly	gly
469	GTG	GGC	TCC	ATC	GTC	CGT	GTC	CTG	ACT	GCA	AGG	AAA
	val	gly	ser	ile	val	arg	val	leu	thr	ala	arg	lys
505	ACC	GTG	TAG	CCT	GGC	AGG	AAC	GGG	TGC	CTG	CCG	GGG
	thr	val										

[illegible]

1	GAC	TGC	CGC	AGC	AGC	AGC	AAC	AAC	CGC	TAG	CCG	AAG
	asp	cys	arg	ser	ser	ser	asn	asn	arg	Xaa	pro	lys
37	GGT	GGC	GCG	GCG	CGG	GCC	GGC	GGC	CCG	GCG	CGG	CCC
	gly	gly	ala	ala	arg	ala	gly	gly	pro	ala	arg	pro
73	GTG	AGC	CTG	CGG	GAA	GTC	GTG	CGC	TAC	CTC	GGG	GGT
	val	ser	leu	arg	glu	val	val	arg	tyr	leu	gly	gly
109	AGC	AGC	GGC	GCT	GGC	GGC	CGC	CTG	ACC	CGC	GGC	CGC
	ser	ser	gly	ala	gly	gly	arg	leu	thr	arg	gly	arg
145	GTG	CAG	GGT	CTG	CTG	GAA	GAG	GAG	GCG	GCG	GCG	CGG
	val	gln	gly	leu	leu	glu	glu	glu	ala	ala	ala	arg
181	GGC	CGC	CTG	GAG	CGC	ACC	CGT	CTC	GGA	GCG	CTT	GCG
	gly	arg	leu	glu	arg	thr	arg	leu	gly	ala	leu	ala
217	CTG	CCC	CGC	GGG	GAC	AGG	CCC	GGA	CGG	GCG	CCA	CCG
	leu	pro	arg	gly	asp	arg	pro	gly	arg	ala	pro	pro
253	GCC	GCC	AGC	GCC	CGC	GCG	GCG	CGG	AAC	AAG	AGA	GCT
	ala	ala	ser	ala	arg	ala	ala	arg	asn	lys	arg	ala
289	GGC	GAG	GAG	CGA	GTG	CTT	GAA	AAG	GAG	GAG	GAG	GAG
	gly	glu	glu	arg	val	leu	glu	lys	glu	glu	glu	glu
325	GAG	GAG	GAG	GAA	GAC	GAC	GAG	GAC	GAC	GAC	GAC	GAC
	glu	glu	glu	glu	asp	asp	glu	asp	asp	asp	asp	asp
361	GTC	GTG	TCC	GAG	GGC	TCG	GAG	GTG	CCC	GAG	AGC	GAT
	val	val	ser	glu	gly	ser	glu	val	pro	glu	ser	asp
397	CGT	CCC	GCG	GGT	GCG	CAG	CAT	CAC	CAG	CTG	AAT	GGC
	arg	pro	ala	gly	ala	gln	his	his	gln	leu	asn	gly
433	GGC	GAG	CGC	GGC	CCG	CAG	ACC	GCC	AAG	GAG	CGG	GCC
	gly	glu	arg	gly	pro	gln	thr	ala	lys	glu	arg	ala
469	AAG	GAG	TGG	TCG	CTG	TGT	GGC	CCC	CAC	CCT	GGC	CAG
	lys	glu	trp	ser	leu	cys	gly	pro	his	pro	gly	gln

Fig. 11 (continued)

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
glu glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
 arg gln val phe ser met ala ala **leu** **ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
 gly gly **ser** ala ser **ser** **thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
 pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
 leu pro gly ala asp gly thr pro phe gly cys pro

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
ala gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
 trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
 ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
 gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
 arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
 gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
 val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

00075740 104304

Fig. 12

256		GCC	AGC	GCC	CGC	GCG	GCG	CGG	AAC	AAG	AGA	GCT
		ala	ser	ala	arg	ala	ala	arg	asn	lys	arg	ala
289	GGC	GAG	GAG	CGA	GTG	CTT	GAA	AAG	GAG	GAG	GAG	GAG
	gly	glu	glu	arg	val	leu	glu	lys	glu	glu	glu	glu
325	GAG	GAG	GAG	GAA	GAC	GAC	GAG	GAC	GAC	GAC	GAC	GAC
	glu	glu	glu	glu	asp	asp	glu	asp	asp	asp	asp	asp
361	GTC	GTG	TCC	GAG	GGC	TCG	GAG	GTG	CCC	GAG	AGC	GAT
	val	val	ser	glu	gly	ser	glu	val	pro	glu	ser	asp
397	CGT	CCC	GCG	GGT	GCG	CAG	CAT	CAC	CAG	CTG	AAT	GGC
	arg	pro	ala	gly	ala	gln	his	his	gln	leu	asn	gly
433	GGC	GAG	CGC	GGC	CCG	CAG	ACC	GCC	AAG	GAG	CGG	GCC
	gly	glu	arg	gly	pro	gln	thr	ala	lys	glu	arg	ala
469	AAG	GAG	TGG	TCG	CTG	TGT	GGC	CCC	CAC	CCT	GGC	CAG
	lys	glu	trp	ser	leu	cys	gly	pro	his	pro	gly	gln
505	GAG	GAA	GGG	CGG	GGG	CCG	GCC	GCG	GGC	AGT	GGC	ACC
	glu	glu	gly	arg	gly	pro	ala	ala	gly	ser	gly	thr
541	CGC	CAG	GTG	TTC	TCC	ATG	GCG	GCC	TTG	AGT	AAG	GAG
	arg	gln	val	phe	ser	met	ala	ala	leu	ser	lys	glu
577	GGG	GGA	TCA	GCC	TCT	TCG	ACC	ACC	GGG	CCT	GAC	TCC
	gly	gly	ser	ala	ser	ser	thr	thr	gly	pro	asp	ser
613	CCG	TCC	CCG	GTG	CCT	TTG	CCC	CCC	GGG	AAG	CCA	GCC
	pro	ser	pro	val	pro	leu	pro	pro	gly	lys	pro	ala
649	CTC	CCA	GGA	GCC	GAT	GGG	ACC	CCC	TTT	GGC	TGC	CCT
	leu	pro	gly	ala	asp	gly	thr	pro	phe	gly	cys	pro
685	GCC	GGG	CGC	AAA	GAG	AAG	CCG	GCA	GAC	CCC	GTG	GAG
	ala	gly	arg	lys	glu	lys	pro	ala	asp	pro	val	glu
721	TGG	ACA	GTC	ATG	GAC	GTC	GTG	GAG	TAC	TTC	ACC	GAG
	trp	thr	val	met	asp	val	val	glu	tyr	phe	thr	glu

Fig. 12 (continued)

757	GCG	GGC	TTC	CCT	GAG	CAA	GCC	ACG	GCT	TTC	CAG	GAG
	ala	gly	phe	pro	glu	gln	ala	thr	ala	phe	gln	glu
793	CAG	GAG	ATC	GAC	GGC	AAG	TCC	CTG	CTG	CTC	ATG	CAG
	gln	glu	ile	asp	gly	lys	ser	leu	leu	leu	met	gln
829	CGC	ACC	GAT	GTC	CTC	ACC	GGC	CTG	TCC	ATC	CGC	CTG
	arg	thr	asp	val	leu	thr	gly	leu	ser	ile	arg	leu
865	GGG	CCA	GCG	TTG	AAA	ATC	TAT	GAG	CAC	CAT	ATC	AAG
	gly	pro	ala	leu	lys	ile	tyr	glu	his	his	ile	lys
901	GTG	CTG	CAG	CAG	GGT	CAC	TTC	GAG	GAC	GAT	GAC	CCG
	val	leu	gln	gln	gly	his	phe	glu	asp	asp	asp	pro
937	GAA	GGC	TTC	CTG	GGA	TGA	GCA	CAG	AGC	CGC	CGC	GCC
	glu	gly	phe	leu	gly							
973	CCT	TGT	CCC	CAC	CCC	CAC	CCC	GCC	TGG	ACC	CAT	TCC
1009	TGC	CTC	CAT	GTC	ACC	CAA	GGT	GTC	CCA	GAG	GCC	AGG
1045	AGC	TGG	ACT	GGG	CAG	GCG	AGG	GGT	GCG	GAC	CTA	CCC
1081	TGA	TTC	TGG	TAG	GGG	GCG	GGG	CCT	TGC	TGT	GCT	CAT
1117	TGC	TAC	CCC	CCC	ACC	CCG	TGT	GTG	TCT	CTG	CAC	CTG
1153	CCC	CCA	GCA	CAC	CCC	TCC	CGG	AGC	CTG	GAT	GTC	GCC
1189	TGG	GAC	TCT	GGC	CTG	CTC	ATT	TTG	CCC	CCA	GAT	CAG
1225	CCC	CCT	CCC	TCC	CTC	CTG	TCC	CAG	GAC	ATT	TTT	TAA
1261	AAG	AAA	AAA	AGG	AAA	AAA	AAA	AAT	TGG	GGA	GGG	GGC
1297	TGG	GAA	GGT	GCC	CCA	AGA	TCC	TCC	TCG	GCC	CAA	CCA
1333	GGT	GTT	TAT	TCC	TAT	ATA	TAT	ATA	TAT	ATG	TTT	TGT
1369	TCT	GCC	TGT	TTT	TCG	TTT	TTT	GGT	GCG	TGG	CCT	TTC
1405	TTC	CCT	CCC	ACC	ACC	ACT	CAT	GGC	CCC	AGC	CCT	GCT
1441	CGC	CCT	GTC	GGC	GGG	AGC	AGC	TGG	GAA	TGG	GAG	GAG
1477	GGT	GGG	ACC	TTG	GGT	CTG	TCT	CCC	ACC	CTC	TCT	CCC
1513	GTT	GGT	TCT	GTT	GTC	GCT	CCA	GCT	GGC	TGT	ATT	GCT
1549	TTT	TAA	TAT	TGC	ACC	GAA	GGG	TTG	TTT	TTT	TTT	TTT
1585	TAA	ATA	AAA	TTT	TAA	AAA	AAG	GAA	AAA	AAA	AAA	AAA

Fig. 13

196 ACC CGT CTC GGA GCG CTT GCG
thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
glu glu glu glu asp asp glu asp asp asp asp asp

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
lys glu trp **ser** leu cys gly pro his **pro** gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
glu glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
arg gln val phe ser met ala ala **leu ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
gly gly **ser** ala ser **ser thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
leu pro gly ala asp gly thr pro phe gly cys pro

Fig. 13 (continued)

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
ala gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
 trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
 ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
 gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
 arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
 gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
 val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG

1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC

1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG

1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA

1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC

1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA

1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT

1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC

1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT

1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG

1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC

1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT

1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT

1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

Fig. 14 (continued)

541 GAA AAG AAG AAG GCC AAG GGT CTG GGA AAG GAG ATC
glu lys lys lys ala lys gly leu gly lys glu ile

577 ACG CTG CTG ATG CAG ACA CTG AAC ACG CTG AGC ACC
thr leu leu met gln thr leu asn thr leu ser thr

613 CCA GAG GAG AAG CTG GCG GCT CTG TGC AAG AAG TAT
pro glu glu lys leu ala ala leu cys lys lys tyr

649 GCG GAA CTG CTC GAG GAG CAC CGG AAC TCG CAG AAG
ala glu leu leu glu glu his arg asn ser gln lys

685 CAG ATG AAG CTG CTG CAG AAG AAG CAG AGC CAG CTG
gln met lys leu leu gln lys lys gln ser gln leu

721 GTG CAG GAG AAG GAC CAC CTG CGT GGC GAG CAC AGC
val gln glu lys asp his leu arg gly glu his ser

757 AAG GCC ATC CTG GCC CGC AGC AAG CTC GAG AGC CTG
lys ala **ile** leu ala arg ser lys leu glu ser leu

793 TGC CGG GAG CTG CAG CGG CAC AAC CGC TCG CTC AAG
cys arg glu leu gln arg his asn arg ser leu lys

829 GAA GAA GGT GTG CAG CGA GCC CGA GAG GAG GAG GAG
glu glu gly val gln arg ala arg glu glu glu glu

865 AAG CGC AAG GAG GTG ACG TCA CAC TTC CAG ATG ACG
lys arg lys glu val thr ser his phe gln **met** thr

901 CTC AAC GAC ATT CAG CTG CAG ATG GAG CAG CAC AAC
leu asn asp ile gln leu gln met glu gln his asn

937 GAG CGC AAC TCC AAG CTG CGC CAG GAG AAC ATG GAG
glu arg asn ser lys leu arg gln glu asn met glu

973 CTG GCC GAG CGG CTC AAG AAG CTG ATT GAG CAG TAC
leu ala glu arg leu lys lys leu ile glu gln tyr

1009 GAG CTG CGA GAA GAG CAC ATC GAC AAA GTC TTC AAA
glu leu arg glu glu his ile asp lys val phe lys

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Fig. 14 (continued)

1045	CAC AAG GAT CTG CAG CAG CAG CTG GTG GAC GCC AAG	his lys asp leu gln gln gln leu val asp ala lys
1081	CTC CAG CAG GCC CAG GAG ATG CTG AAG GAG GCA GAG	leu gln gln ala gln glu met leu lys glu ala glu
1117	GAG CGG CAC CAG CGG GAG AAG GAC TTT CTC CTG AAG	glu arg his gln arg glu lys asp phe leu leu lys
1153	GAG GCC GTG GAG TCC CAG AGG ATG TGC GAG CTG ATG	glu ala val glu ser gln arg met cys glu leu met
1189	AAG CAA CAG GAG ACC CAC CTG AAG CAG CAG CTT GCC	lys gln gln glu thr his leu lys gln gln leu ala
1225	CTA TAC ACA GAG AAG TTT GAG GAG TTC CAG AAC ACT	leu tyr thr glu lys phe glu glu phe gln asn thr
1261	CTT TCC AAA AGC AGC GAG GTG TTC ACC ACA TTC AAA	leu ser lys ser ser glu val phe thr thr phe lys
1297	CAG GAA ATG GAA AAG ATG ACA AAG AAG ATC AAG AAG	gln glu met glu lys met thr lys lys ile lys lys
1333	CTG GAG AAA GAG ACC ACC ATG TAC CGT TCC CGG TGG	leu glu lys glu thr thr met tyr arg ser arg trp
1369	GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG	glu ser ser asn lys ala leu leu glu met ala glu
1405	GAG AAA ACA CTC CGG GAC AAA GAG CTG GAA GGC CTG	glu lys thr leu arg asp lys glu leu glu gly leu
1441	CAG GTG AAA ATC CAG CGG CTG GAG AAG CTG TGC CGG	gln val lys ile gln arg leu glu lys leu cys arg
1477	GCA CTG CAG ACA GAG CGC AAT GAC CTG AAC AAG AGG	ala leu gln thr glu arg asn asp leu asn lys arg
1513	GTG CAG GAC CTG AGT GCC GGT GGC CAG GGC CCC GTC	val gln asp leu ser ala gly gly gln gly pro val

Fig. 14 (continued)

2665	AGA	AGA	GGC	GTC	TGA	TGG	CTT	TGC	CGC	CAG	CTT	GCC
2701	TGC	GGG	CCT	CAA	TCC	CGG	GAG	GCC	GCC	CGG	TTC	CCG
2737	TCA	CTG	TTG	TCC	CCG	TGC	AGT	GCG	TTG	CTG	GTC	CCC
2773	AGG	ACC	AGC	TGC	TCG	TTT	GCT	GTA	TGG	GTC	AGT	TTC
2809	TGC	TTC	CTG	CCC	CCC	ACT	CCA	CCT	AAC	TGC	AAT	CCT
2845	TGG	GGT	TTC	CCT	GGT	TCT	CGT	CCC	TGG	TAC	CTC	TGT
2881	GCC	CAA	GAA	GTA	GCC	TTC	TTT	GGG	ATT	CTT	GTT	CTG
2917	CCC	ATG	CGG	GAG	CTG	CTG	CTG	TCT	GAC	AGG	TGA	GGC
2953	CTG	AGA	CTC	AGC	GGC	TGA	CAG	AGC	TGC	AGA	GCT	CTG
2989	CAC	GGT	GGC	TCC	CGG	GGC	GGC	CTC	TGT	GTG	CTG	CAC
3025	ACC	GCT	GCT	CTG	CTG	GCA	CTG	GCC	AGT	CTG	TGC	AGA
3061	GCA	TTT	GAG	TAC	TGG	CTC	AGG	AGG	GAG	GGC	TCT	GCT
3097	GGC	CTC	GAG	GGA	CAG	CGC	CAC	GTC	TCC	AGC	TGG	GCT
3133	CAG	GGA	GAG	CCC	CAG	ACT	GGC	TGC	GTA	GGG	TGC	TTG
3169	GGG	TTT	GCT	TCT	TGC	AGT	ATT	TCT	TGG	AAG	CTG	TTT
3205	TGT	TGT	CCT	GCT	ATT	CCT	TCA	TCT	TCC	ACA	GTC	CAC
3241	GCT	CAG	CCT	TTA	ACT	TGG	ATC	CCT	CAC	ATA	ACA	GGG
3277	TTC	ATG	AGA	CCC	GCA	AGT	ACG	CCC	AAG	CTA	CGT	ATG
3313	GCT	GAG	GCC	AGC	TGG	CAG	GTG	AAT	GGC	ACG	CCA	TTG
3349	CTG	CTG	CTA	ATC	CCT	GGC	ATA	TCT	TTA	GTT	CAC	CTC
3385	GAA	ATG	CCC	CCG	CCA	CAG	TGC	AAG	CAG	TGA	GTC	CAC
3421	GTG	CCA	CCC	TGG	GCT	GAA	TCC	CAC	CCC	CTG	TGA	GTG
3457	TTG	CCC	GAG	ATT	GTG	TCT	CTT	CTG	AAT	GCC	TTC	ACT
3493	GGG	AAT	GGC	CTC	TGC	CGC	CTC	CTG	CTC	AGG	GAG	GCT
3529	TTC	CCC	TTC	CCT	CAG	CCC	CTG	TGC	CAG	ACT	GAG	GTA
3565	CAA	GAA	CCG	CCA	AGC	CCA	TGC	AAG	GTG	TGG	CTA	GGC
3601	GCC	AGG	GTG	CAG	GAA	GGA	GGC	AGG	TAG	CTG	CCT	GCA
3637	CCC	TTG	AAA	GCC	AAG	AGG	CCT	ACG	GTG	GCC	TCC	ATC
3673	CTG	GCT	TGC	CTC	ACT	TCA	GCT	ACC	TCG	CAT	AGC	CCA
3709	GGG	GTG	GGG	CTA	TTG	GAT	TCC	AGG	GTG	GGG	GGA	TGG
3745	GAA	GCT	GCA	GGG	GGC	AGG	TGG	CTC	TCA	CTA	GGC	TTC
3781	CCA	GCT	CAG	GAA	TGT	GGG	CCT	CAG	GTA	GGG	GAG	AGC
3817	CTT	TGC	TCC	ACT	CCA	CCC	ATT	TGC	AGG	CAT	CTA	GGC
3853	CAG	TCT	AGA	TGG	CGA	CCC	CTT	CTC	TTC	CTC	TCC	ATT
3889	GAC	CAA	ATC	GTA	CCT	GTC	TCT	CCA	GCT	GCT	CGC	TTG
3925	CTC	TGC	TTT	CCA	AAG	TCA	GCC	CAG	GTA	CCC	AGG	TGC
3961	CGC	CCA	CAT	TGG	CCT	GGA	ACC	TGG	ACC	AGA	GGC	AAG
3997	GGA	GGT	GGC	CTA	TCC	TTG	AGT	GAT	AGC	CAG	TGC	CTT
4033	CCT	CAC	CCG	GTG	GCT	TCC	ATG	CCT	GTG	ACC	TCA	GAT
4069	TTA	GGA	CCA	AGA	GCT	GTG	TTG	GTT	TCT	TAC	GTT	GTG
4105	AGC	TTT	CCC	TCC	AGG	GGA	CCA	CAG	CAG	GTG	AGG	CTC
4141	GGA	GCC	CAG	AGC	CCT	TGG	CGC	CGC	CAG	CAG	TAA	CTT
4177	GTG	TCC	GGA	CCT	TGT	CCA	GCT	GAG	CGC	TTC	GTG	TAT

Fig. 15

1 GAC GCC TCA GAG CGG AAC AGG GAA GTG AAT CAG GCG
 37 CCG GGT AGT GGG TTG CTG GGC TGG GCT TGC TGA GGT
 73 AGA GGC AGC GCC AAG AAG AGG CCT TTG CCG CTG GTC
 109 GGG ATT GGG ATG TCG AAG AAC ACA GTG TCG TCG GCC
 met ser lys asn thr val ser ser ala

 145 CGC TTC CGG AAG GTG GAC GTG GAT GAA TAT GAC GAG
 arg phe arg lys val asp val asp glu tyr asp glu

 181 AAC AAG TTC GTG GAC GAA GAA GAT GGG GGC GAC GGC
 asn lys phe val asp glu glu asp gly gly asp gly

 217 CAG GCC GGG CCC GAC GAG GGC GAG GTG GAC TCC TGC
 gln ala gly pro asp glu gly glu val asp ser cys

 253 CTG CGG CAA GGA AAC ATG ACA GCT GCC CTA CAG GCA
 leu arg gln gly asn met thr ala ala leu gln ala

 289 GCT CTG AAG AAC CCC CCT ATC AAC ACC AAG AGT CAG
 ala leu lys asn pro pro ile asn thr **lys** ser gln

 325 GCA GTG AAG GAC CGG GCA GGC AGC ATT GTC TTG AAG
 ala val lys asp arg ala gly ser ile val leu lys

 361 GTG CTC ATC TCT TTT AAA GCT AAT GAT ATA GAA AAG
 val leu ile ser phe lys ala **asn** asp ile glu lys

 397 GCA GTT CAA TCT CTG GAC AAG AAT GGT GTG GAT CTC
 ala val gln ser leu asp **lys** asn gly val asp leu

 433 CTA ATG AAG TAT ATT TAT AAA GGA TTT GAG AGC CCG
 leu met lys tyr ile tyr lys gly phe glu ser pro

 469 TCT GAC AAT AGC AGT GCT ATG TTA CTG CAA TGG CAT
 ser asp asn ser ser ala **met** leu leu gln trp his

 505 GAA AAG GCA CTT GCT GCT GGA GGA GTA GGG TCC ATT
 glu lys ala leu ala ala gly gly val gly ser ile

 541 GTT CGT GTC TTG ACT GCA AGA AAA ACT GTG TAG TCT
 val arg val leu thr ala arg lys thr val

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

Fig. 16

1 GAA GAG CGA GTA CTT GAG AAA GAA GAG GAA GAA GAT
glu glu arg val leu glu lys glu glu glu glu **asp**

37 GAT GAT GAA GAT GAA GAT GAA GAA GAT GAT GTG TCA
asp asp glu asp **glu asp** glu glu asp asp val ser

73 GAG GGC TCT GAA GTG CCC GAG AGT GAC CGT CCT GCA
glu gly ser glu val pro glu ser asp arg pro ala

109 GGT GCC CAG CAC CAC CAG CTT AAC GGC GAG CGG GGA
gly ala gln his his gln leu asn gly glu arg gly

145 CCT CAG AGT GCC AAG GAG AGG GTC AAG GAG TGG ACC
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**

181 CCC TGC GGA CCG CAC CAG GGC CAG GAT GAA GGG CGG
pro cys gly pro his **gln** gly gln **asp** glu gly arg

217 GGG CCA GCC CCG GGC AGC GGC ACC CGC CAG GTG TTC
gly pro ala **pro** gly ser gly thr arg gln val phe

253 TCC ATG GCA GCC ATG AAC AAG GAA GGG GGA ACA GCT
ser met ala ala **met asn** lys glu gly gly **thr** ala

289 TCT GTT GCC ACC GGG CCA GAC TCC CCG TCC CCC GTG
ser **val ala** thr gly pro asp ser pro ser pro val

325 CCT TTG CCC CCA GGC AAA CCA GCC CTA CCT GGG GCC
pro leu pro pro gly lys pro ala leu pro gly ala

361 GAC GGG ACC CCC TTT GGC TGT CCT CCC GGG CGC AAA
asp gly thr pro phe gly cys pro **pro** gly arg lys

397 GAG AAG CCA TCT GAT CCC GTC GAG TGG ACC GTG ATG
glu lys pro **ser** asp pro val glu trp thr val met

433 GAT GTC GTC GAA TAT TTT ACT GAG GCT GGA TTC CCG
asp val val glu tyr phe thr glu ala gly phe pro

469 GAG CAG GCG ACA GCT TTC CAA GAG CAG GAA ATT GAT
glu gln ala thr ala phe gln glu gln glu ile asp

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Fig. 16 (continued)

505 GGC AAA TCT TTG CTG CTC ATG CAG CGC ACA GAT GTG
gly lys ser leu leu leu met gln arg thr asp val

541 CTC ACC GGC CTG TCC ATC CGC CTC GGG CCA GCC CTG
leu thr gly leu ser ile arg leu gly pro ala leu

577 AAA ATC TAC GAG CAC CAC ATC AAG GTG CTT CAG CAA
lys ile tyr glu his his ile lys val leu gln gln

613 GGC CAC TTT GAG GAT GAT GAC CCC GAT GGC TTC TTA
gly his phe glu asp asp asp pro **asp** gly phe leu

649 GGC TGA GCG CCC AGC CTC ACC CCT GCC CCA GCC CAT
gly

685 TCC GGC CCC CAT CTC ACC CAA GAT CCC CCA GAG TCC

721 AGG AGC TGG ACG GGG ACA CCC TCA GCC CTC ATA ACA

757 GAT TCC AAG GAG AGG GCA CCC TCT TGT CCT TAT CTT

793 TGC CCC TTG TNT CTG TCT CAC ACA CAT CTG CTC CTC

829 AGC ACG TCG GTG TGG GGA GGG GAT TGC TCC TTA AAC

865 CCC AGG TGG CTG ACC CTC CCC ACC CAG TCC AGG ACA

901 TTT TAG GAA AAA AAA AAT GAA ATG TGG GGG GCT TCT

937 CAT CTC CCC AAG ATC CTC TTC CGT TCA GCC AGA TGT

973 TTC CTG TAT AAA TGT TTG GAT CTG CCT GTT TAT TTT

1009 GGT GGG TGG TCT TTC CTC CCT CCC CTA CCA CCC ATG

1045 CCC CCC TTC TCA GTC TGC CCC TGG CCT CCA GCC CCT

1081 AGG GGA CTA GCT GGG TTG GGG TTC CTC GGG CCT TTT

1117 CTC TCC TCC CTC TTT TCT TTC TGT TGA TTG TCG CTC

1153 CAG CTG GCT GTA TTG CTT TTT AAT ATT GCA CCG AAG

1189 GTT TTT TAA ATA AAA TTT TA

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Variable	Mean	Standard Deviation	Minimum	Maximum
Age	35.2	12.5	18	65
Gender	0.45	0.50	0	1
Marital Status	0.60	0.49	0	1
Education	12.5	2.1	9	16
Income	45000	15000	20000	80000
Health	0.75	0.43	0	1
Smoking	0.30	0.46	0	1
Alcohol	0.20	0.40	0	1
Exercise	0.10	0.30	0	1
Stress	0.50	0.50	0	1
Sleep	0.60	0.49	0	1
Appetite	0.70	0.46	0	1
Mood	0.80	0.41	0	1
Energy	0.90	0.29	0	1
Concentration	0.85	0.36	0	1
Memory	0.80	0.41	0	1
Emotion	0.70	0.46	0	1
Behavior	0.60	0.49	0	1
Thought	0.50	0.50	0	1
Feeling	0.40	0.50	0	1
Perception	0.30	0.46	0	1
Attention	0.20	0.40	0	1
Intuition	0.10	0.30	0	1
Imagination	0.05	0.22	0	1
Reason	0.00	0.00	0	0

1	CA	AAA	AGC	AGC	CCA	GGA	CAA	CCG	GAA	GCA	GGA	CCC	GAG	GGA	GCC
	lys	ser	ser	pro	gly	gln	pro	glu	ala	gly	pro	glu	gly	ala	
45	CAG	GAG	CGG	CCC	AGC	CAG	GCG	GCT	CCT	GCA	GTA	GAA	GCA	GAA	GGT
	gln	glu	arg	pro	ser	gln	ala	ala	pro	ala	val	glu	ala	glu	gly
90	CCC	GGC	AGC	AGC	CAG	GCT	CCT	CGG	AAG	CCG	GAG	GGG	GCT	CAA	GCC
	pro	gly	ser	ser	gln	ala	pro	arg	lys	pro	glu	gly	ala	gln	ala
135	AGA	ACG	GCT	CAG	TCT	GGG	GCC	CTT	CGT	GAT	GTC	TCT	GAG	GAG	CTG
	arg	thr	ala	gln	ser	gly	ala	leu	arg	asp	val	ser	glu	glu	leu
180	AGC	CGC	CAA	CTG	GAA	GAC	ATA	CTG	AGC	ACA	TAC	TGT	GTG	GAC	AAT
	ser	arg	gln	leu	glu	asp	ile	leu	ser	thr	tyr	cys	val	asp	asn
225	AAC	CAG	GGG	GGC	CCC	GGC	GAG	GAT	GGG	GCA	CAG	GGT	GAG	CCG	GCT
	asn	gln	gly	gly	pro	gly	glu	asp	gly	ala	gln	gly	glu	pro	ala
270	GAA	CCC	GAA	GAT	GCA	GAG	AAG	TCC	CGG	ACC	TAT	GTG	GCA	AGG	AAT
	glu	pro	glu	asp	ala	glu	lys	ser	arg	thr	tyr	val	ala	arg	asn
315	GGG	GAG	CCT	GAA	CCA	ACT	CCA	GTA	GTC	TAT	GGA	GAG	AAG	GAA	CCC
	gly	glu	pro	glu	pro	thr	pro	val	val	tyr	gly	glu	lys	glu	pro
360	TCC	AAG	GGG	GAT	CCA	AAC	ACA	GAA	GAG	ATC	CGG	CAG	AGT	GAC	GAG
	ser	lys	gly	asp	pro	asn	thr	glu	glu	ile	arg	gln	ser	asp	glu
405	GTC	GGA	GAC	CGA	GAC	CAT	CGA	AGG	CCA	CAG	GAG	AAG	AAA	AAA	GCC
	val	gly	asp	arg	asp	his	arg	arg	pro	gln	glu	lys	lys	lys	ala
450	AAG	GGT	TTG	GGG	AAG	GAG	ATC	ACG	TTG	CTG	ATG	CAG	ACA	TTG	AAT
	lys	gly	leu	gly	lys	glu	ile	thr	leu	leu	met	gln	thr	leu	asn
495	ACT	CTG	AGT	ACC	CCA	GAG	GAG	AAG	CTG	GCT	GCT	CTG	TGC	AAG	AAG
	thr	leu	ser	thr	pro	glu	glu	lys	leu	ala	ala	leu	cys	lys	lys
540	TAT	GCT	GAA	CTG	CTG	GAG	GAG	CAC	CGG	AAT	TCA	CAG	AAG	CAG	ATG
	tyr	ala	glu	leu	leu	glu	glu	his	arg	asn	ser	gln	lys	gln	met
585	AAG	CTC	CTA	CAG	AAA	AAG	CAG	AGC	CAG	CTG	GTG	CAA	GAG	AAG	GAC
	lys	leu	leu	gln	lys	lys	gln	ser	gln	leu	val	gln	glu	lys	asp
630	CAC	CTG	CGC	GGT	GAG	CAC	AGC	AAG	GCC	GTC	CTG	GCC	CGC	AGC	AAG
	his	leu	arg	gly	glu	his	ser	lys	ala	val	leu	ala	arg	ser	lys
675	CTT	GAG	AGC	CTA	TGC	CGT	GAG	CTG	CAG	CGG	CAC	AAC	CGC	TCC	CTC
	leu	glu	ser	leu	cys	arg	glu	leu	gln	arg	his	asn	arg	ser	leu

Fig. 17 (continued)

720 AAG GAA GAA GGT GTG CAG CGG GCC CGG GAG GAG GAG GAG AAG CGC
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg

765 AAG GAG GTG ACC TCG CAC TTC CAG GTG ACA CTG AAT GAC ATT CAG
lys glu val thr ser his phe gln val thr leu asn asp ile gln

810 CTG CAG ATG GAA CAG CAC AAT GAG CGC AAC TCC AAG CTG CGC CAA
leu gln met glu gln his asn glu arg asn ser lys leu arg gln

855 GAG AAC ATG GAG CTG GCT GAG AGG CTC AAG AAG CTG ATT GAG CAG
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln

900 TAT GAG CTG CGC GAG GAG CAT ATC GAC AAA GTC TTC AAA CAC AAG
tyr glu leu arg glu glu his ile asp lys val phe lys his lys

945 GAC CTA CAA CAG CAG CTG GTG GAT GCC AAG CTC CAG CAG GCC CAG
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln

990 GAG ATG CTA AAG GAG GCA GAA GAG CGG CAC CAG CGG GAG AAG GAT
glu met leu lys glu ala glu glu arg his gln arg glu lys asp

1035 TTT CTC CTG AAA GAG GCA GTA GAG TCC CAG AGG ATG TGT GAG CTG
phe leu leu lys glu ala val glu ser gln arg met cys glu leu

1080 ATG AAG CAG CAA GAG ACC CAC CTG AAG CAA CAG CTT GCC CTA TAC
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr

1125 ACA GAG AAG TTT GAG GAG TTC CAG AAC ACA CTT TCC AAA AGC AGC
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

1170 GAG GTA TTC ACC ACA TTC AAG CAG GAG ATG GAA AAG ATG ACT AAG
glu val phe thr thr phe lys gln glu met glu lys met thr lys

1215 AAG ATC AAG AAG CTG GAG AAA GAA ACC ACC ATG TAC CGG TCC CGG
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg

1260 TGG GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG GAG AAA
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys

1305 ACA GTC CGG GAT AAA GAA CTG GAG GGC CTG CAG GTA AAA ATC CAA
thr val arg asp lys glu leu glu gly leu gln val lys ile gln

1350 CGG CTG GAG AAG CTG TGC CGG GCA CTG CAG ACA GAG CGC AAT GAC
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp

1395 CTG AAC AAG AGG GTA CAG GAC CTG AGT GCT GGT GGC CAG GGC TCC
leu asn lys arg val gln asp leu ser ala gly gly gln gly **ser**

1440 CTC ACT GAC AGT GGC CCT GAG AGG AGG CCA GAG GGG CCT GGG GCT
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala

Fig. 17 (continued)

1485 CAA GCA CCC AGC TCC CCC AGG GTC ACA GAA GCG CCT TGC TAC CCA
gln ala pro **ser** ser pro **arg** val thr glu ala pro cys **tyr** pro

1530 GGA GCA CCG AGC ACA GAA GCA TCA GGC CAG ACT GGG CCT CAA GAG
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu

1575 CCC ACC TCC GCC AGG GCC TAG AGA GCC TGG TGT TGG GTC ATG CTG
pro thr **ser** ala **arg** ala ***

1620 GGA AGG GAG CGG CAG CCC AGC CAG GCC TGG CCC ATA AAA GGC TCC
1665 CAT GCT GAG CAG CCC ATT GCT GAA GCC AGG ATG TTC TTG ACC TGG
1710 CTG GCA TCT GGC ACT TGC AAT TTT GGA TTT TGT GGG TCA GTT TTA
1755 CGT ACA TAG GGC ATT TTG CAA GGC CTT GCA AAT GCA TTT ATA CCT
1800 GTA AGT GTA CAG TGG GCT TGC ATT GGG GAT GGG GGT GTG TAC AGA
1845 TGA AGT CAG TGG CTT GTC TGT GAG CTG AAG AGT CTT GAG AGG GGC
1890 TGT CAT CTG TAG CTG CCA TCA CAG TGA GTT GGC AGA AGT GAC TTG
1935 AGC ATT TCT CTG TCT GAT TTG AGG CTC AGA CCC CTC CCT GCC CTT
1980 TCA GAG CTC AAA ACA AGT AAT ACA CCA AGG TCT TGA CTG CAT TTG
2025 TCT TGT GAG CAG GGC TTG CTT GGT CAG CTC AGG CCC TCC TAG CTG
2070 CTT GGA GGC TCC TTT GAT TCT CTA GAC CTG GAA AAG GTG TCC CTA
2115 GGC AGA GCC CTG GCA GGG CGC TCA GAG CTG GGA TTT CCT GCC TGG
2160 AAC AAG GGA CCT GGA GAA TGT TTT TGC GTG GGA TGA TGT GCT GGT
2205 CAG GAG CCC CTT GGG CAT CGC TTC CCC TGC CCT TTG GTA GTG CCA
2250 GGA CCA GGC CAA TGA TGC TTC TCA GTA GCC TTA TCA TTC ACA GGT
2295 GCC TCT CTA GCC TGC ACA AAT GAT TGA CAA GAG ATC ACC CAA AGG
2340 ATT ATT TCT GAA GGT GTT TTT TTC TTT ATT TCT TTT TCT TTT TTT
2385 TTT TTT CTT TTT CTT TTT TTT TTG CAC ATG ACA GTG TTT GTA TTG
2430 AGG ACC TTC CAA GGA AAA GGG ATG CTG TAC CAG TGG TGC CTG GGT
2475 GCC TGG CCT CCA GTG TCC CAC CTC CTT CAC CAC CCC ACT TGG CTC
2520 CTT TGC CAT CTT GAT GCT GAG GTT TCC TGT TTG GTG AGA TCA GGT
2565 TGT TTG TGG TAA AAG AAA GGA AAG GGC TTC TGA TGG CTT TGC CAC
2610 AAG CTT ACC TGT GGG TTT CAG TCC TGA GAG GCC ACC ACC AGT TCC
2655 CAT CAG CAC TGT CTC CAT GCA GCA GTT GCT GGG TCC CAT GTC CAG
2700 CTG CCT CTT TGG CTT CAT GGG TTT TTC TGC TTC CTG CCC CCA CCC
2745 CCA CAT GTG CAA TCC TCA AGA TTT GTC CTG ATT CTA TTT CCT GGC
2790 ACC TCC CTG CCT GTC CTT GGG GAT TCT ACT TCT TCC TGT GTG GGG
2835 CCC ATA GCT GTT GTC TAA CAG GTA AGA AAT GAA ATT GAA CTA TTG
2880 ACT GGG CCC CAG AAA TCC ATA AAA TGG CTG CAG ACA GTT GTT TCT
2925 GTG TCC TGT TCT ACC CCC ACT CCA GTA CAT AAC TAC TAT GTA CTG
2970 TGT AGA GCC ATT CTA TAT GCT GAA TGT TCT GCT GTT GCA AAC TTG
3015 CCA GGG TAT TAG CCA GTG TTT GTG CCA AGC AGT TTT CGG GGA CAA
3060 CAG AAT GAC TCA GAC CAA GAT GGA TAG GAT GGT TAG GGC TTT GCT
3105 TCT TGC TGT TTT TCT TTG AAC TAG TCA TTG TCC TGC AGG TCC CTT
3150 CAT CTT CCA TAC CTA GCC CAC TCT TTT AGC CCT TAC CTT AAA TCT
3195 CTC AGA TAA GTT GGT TCA CAA AGA ATG TTA AGT ACT GAA TCA TGT
3240 GTG ACT GAG ACC AGA GAT GGC AAA TGA ATG GCA CAC CAT TTC TCC
3285 TTC TCC TGC CCC AGG GCA GGT ACC ACT GAT CTG CAT CAG AGT TGC
3330 CTG CTA TTC TCT GGT GTA TCC TTC ACA TCT AGG TGC CCT CAA GCA
3375 GCT GTG TGA GTG TTG AGA TCT CTG CCA TCT CTG GCT GAG ATA CTG
3420 CTG TCC TGT GAA GTG TTT CCC ATG ACC TTT TTC TTC CCC TTT GAA
3465 TCC CTC TTG TCT GGA GTA GTC CTT GCC TTC TTC TTG CTC CAG TAG

Fig. 17 (continued)

3510 GCC TTT TCC TTA CCC CAG CCC TTG TGC CAG GCT AAG CTG GTA CAA
3555 GAG CTG CCA ACT CAC AGA GTT TTG CTA GGC GAG AGA GGT GCA GGG
3600 AAG AGG CAG AGG TAT GCA CCT TCC CCC TTG AAG AGA GGG GAA AGG
3645 CCT ACA GTG GCC CAC ATA ATT GCC TGA CTC ACA CTT CAG CTA CCT
3690 CTT AAT GCC TGT GGA GGG ACT GGA GCT GCT GGA TCC CAG TGT GGT
3735 GGT GTA GGA GGC CAC AGT GAG CAG GTG GCC CCA GCT GGG TTT CCC
3780 AGG TCA GGA ATG TGG GCC CCA GGC AAG GTG CAG CCT TTG CTC ACA
3825 GCT CCA TCC ATG TCT AGA CCT TCA GGC CAG TCT GCA GAT GAG GTT
3870 CCC TAC CTT TTT CTT CTC TTC ATT GAC CAA ATC AAC CAA TCA CTA
3915 CAG CTG CTC TGC TTC TGC TTT CCA AAG TAG CCC AGG TCC TGG GCC
3960 AGA TGC AGG GGA GGT GCC TAT CCA TGA GTG AAG GCC AGT GTC TTC
4005 CTC ACC TGG GTG GTC CCA CAC TTG TGA CCC TCA GTT TTA GGA CCC
4050 AAG ATC TGT GTT GGT TTC TTA GAT TGC TAG CTT TTC CTC CAG GGG
4095 ACC ACA GCA GGT GAA GCT CAA GAG CGC ATG GCT CTG CTA ATA GTA
4140 AAT TGT TTT CAG GGC CTT GTC CAG CTG AGA GCT TCA TGT CCA CCA
4185 GAT TCT GAG AGG TGT CAG CAG CAC TTT TTT TTT TTA TTT GTT GTT
4230 TGT TTT CCA TGA GGT TAT CGG ACC ATG GGC TGA GCT CAG GCA CTT
4275 TCT GTA GGA GAC TGT TAT TTC TGT AAA GAT GGT TAT TTA ACC CTC
4320 CTC CAC CCC ATC ACG GTG GCC CTG AGG GCT GAC CCG GAG GCC AGT
4365 GGA GCT GCC TGG TGT CCA CGG GGG AGG GCC AAG GCC TGC TGA GCT
4410 GAT TCT CCA GCT GCT GCC CCA GCC TTT CCG CCT TGC ACA GCA CAG
4455 AGG TGG TCA CCC CAG GGA CAG CCA GGC ACC TGC TCC TCT TGC CCT
4500 TCC TGG GGG AAA GGA GCT GCC TTC TGT CCC TGT AAC TGC TTT CCT
4545 TAT GGC CCA ACC CGG CCA CTC AGA CTT GTT TGA AGC TGC ACT GGC
4590 AGC TTT TTT GTC TCC TTT GGG TAT TCA CAA CAG CCA GGG ACT TGA
4635 TTT TGA TGT ATT TTA AAC CAC ATT AAA TAA AGA GTC TGT TGC CTT
4680 AAA AAA AAA AAA AAA AAA

3510 3555 3600 3645 3690 3735 3780 3825 3870 3915 3960 4005 4050 4095 4140 4185 4230 4275 4320 4365 4410 4455 4500 4545 4590 4635 4680

Fig. 18

GTG GAC GTG GAT GAG TAC GAC GAG AAC AAG TTC GTG
val asp val asp glu tyr asp glu asn lys phe val

GAC GAG GAA GAC GGC GGC GAC GGC
asp glu glu asp gly gly asp gly

Table 1. Demographic characteristics of the study population	
Age (years)	Mean (SD)
Male	55.2 (10.5)
Female	56.8 (11.2)
Marital status	
Married	78.5%
Single	12.3%
Divorced	5.2%
Widowed	4.0%
Education level	
High school or less	65.8%
College	25.5%
Postgraduate	8.7%
Occupation	
Professional	32.1%
Managerial	18.9%
Technical	15.4%
Service	22.3%
Unemployed	11.3%
Income (TL/month)	
< 1000	15.2%
1000-2000	28.7%
2000-3000	22.5%
> 3000	33.6%
Health status	
Good	72.4%
Fair	18.9%
Poor	8.7%
Smoking status	
Smoker	35.6%
Non-smoker	64.4%
Alcohol consumption	
Regular	12.1%
Occasional	25.3%
Never	62.6%

Fig. 19

	1					50
Rabbit	MSKNTVSSAR	FRKVDVDEYD	ENKFVDEEDG	GDGQAGPDEG	EVDSCLRQGN	
Human	
	51					100
Rabbit	MTAALQAALK	NPPINTRSQA	VKDRAGSIVL	KVLISFKAGD	IEKAVQSLDR	
HumanK...N.K	
	101					150
Rabbit	NGVDLLMKYI	YKGFESPSDN	SSAVLLQWHE	KALAAGGVGS	IVRVLTARKT	
HumanM.....	
	151					
Rabbit	V					
Human	.					

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Fig. 22 (1/5)

1 AAGCTTTATAAAGATTTAACTACCTAATAAGGTAGAGAAGTAATTTATGTGCCCACTAAA 60
 61 AAATACTCAATTTCTGAATGTTTCGTCCAAAATTAACCTGTGAGATCATTAAATCATTGAC 120
 121 TAGAAACACGTTGAGTACCTATTATGTACTAGGCACTTAGATCATTGTGAGACAATAAAA 180
 181 AATACTGCATTAGAAAAGGACATTTTTTACATCTTAAATGCAATAAGCATTATTTGGCTG 240
 241 GCAGTTAATTACATTTAACACATTAACATATAGAGCAAAATCTGAGCAATCAAAAATAA 300
 301 TTATACCTTTGAGCAATCGATTATTTAAATTTCTTCACTATTCCCTTAAGCTGATTCT 360
 361 ACTCTGGGATTCTTTCATAGTTCTCAAATAAGAAAATAAAAAATTTCTTAAATAAGGCAA 420
 421 TACAAAAGAATAGAAATGTAAGAGAAGAGATATATTAGCTCTTGAATCCCTGTTTCCATT 480
 481 TGCTGTCAATAGTGCCTCTAATGTTTCGATTTTCTCTTCAAAGAAAAATCTTGATTTAAA 540
 541 GGAAGAAAAAGTACAATCACCTTTAACAGCTAAAGTATACTGATTAGCATCTACTAAAGT 600
 601 TAGCAAAGACTGAAACTGAAAAAAATTTGTAATCTTTATTCTAAGTTATATAACGCCA 660
 661 TTCACCATAGTAATGATTTTATACTTTGGTATATGGCTTTTTTAAAAATAAATATTGCCAAC 720
 721 AGGTAAAAATTTTTCTTTGCTGTCTTAAGGCATTCTTAAGAGAATTTTTTACCAGTGTGT 780
 781 GTTCATAACTTGAATGTTAATTTAAACAATGTTACTTCTATCACCTAAATGATATACTTA 840
 841 TAGAAGAGTGGTTTAATTGGGAACAGAAAAACACCACATTGCTTCTTCCCAAGAAAAAGG 900
 901 GATGTATTCCATTCTCGAGGTCTCTCTCCCACTCTCTATTTATATATAATATACTGCATA 960
 961 GATAAATATACACACATTATATATGTATTTTTTTGAACTTAAAGAAGACTGGACATATGT 1020
 1021 ATTTACATGTATATATCCAACAAATTTAATTTTGAGATCTCTCTCCCTCTTCTGATTT 1080
 1081 ATTATTCTCAGTATGAATTTCTCAAATGTACGGTCTTTTACATTTCAATTCATTCAAG 1140
 1141 CATGTATCGAGTCCCTTCTGCATGCTTAGCTTTTTTGTATATGGAAGGAAGATACAAAAG 1200
 1201 AAAAAGTGTCTTCTGCCCTTCAGAATCTTTCCATCTCTTCTAGGAAGGAGATAAAACACCA 1260
 1261 TATATCATTAAGAAATTTATAAGACTAGTCCCAAAACCAATGGTACAAGCAACATGCATT 1320
 1321 TTACATTTATGTAGAATTTTAGAGCTTGGAAACACTTTCGTGATATATAATCCTAAGAAC 1380
 1381 AATCTTGTAAGTGCACATTATTAGCTCCATTTTCACTGATGAGGAATCTGAGACAGAATT 1440
 1441 TTAAGTGACATGTCTCGTTCAAACATTATGAGTGAAGAGTCAACACTTAAGCCTGAGTT 1500
 1501 TTCTGATTCTAAGCCTAGTGCTCTTTTCAACACAGCACTGGAAACCAAAGATTGTGGTAC 1560
 1561 ACAACAAGGCAACAGCCAGTCTTCTTGCTCGAGGTCCAACCTAACTGGACCCATACCGAG 1620
 1621 CAGTGTCCAGCCAAATGTCCAAATTAATTTTATCCTGCAATATTTGTTCTTCACTGTAA 1680
 1681 TACACACAGCACAACTACCATTTCTTCTGCTTAGTGCCTTTATCTCTTACATTCCAGAA 1740
 1741 ATGGGGATGTCAAATATTTTTTTTAAATCTGGCCTAGATGGAATCATATAAATCTCAAATC 1800
 1801 ATAATATAAATCTTAAAGGTCTGGTTTCCACCAATCCTTCCACATTTTGTTTTCCCCCAG 1860
 1861 CACTAGAGAGCCTAACCTACCCTCACCCCTTTCGAGCATTCTTGCTCCAAACGACCACCT 1920
 1921 ATTTTAAGATGTCAATGACCCTTTCCCAAATTTCTACAAATTCACCCAGTTTGGCCACC 1980
 1981 GACCCAGCGCCTGCCCGGACACGTTCCCTCCCTCCCAATAGATTTGATACCGAGTTCA 2040
 2041 GGTCTGTCAGATCCCGTTGCGATGCTGTACACAGCACTGACAGATAAGATTTGACCTTT 2100
 2101 CGACTCCGTCCTTGGGGACTTCCCGCTGGCCAGGAAGGGTAGTTCCAATCCAGGAAACG 2160
 2161 GGCTTCCTGCTCAGGAACGCAGCCTCTAGCAGCGACAGTCTGAGGCAATGTCTCCGGCA 2220
 2221 ATTAGAACGATGCTGGGCGCCCGGGTGTGCATCACTCTGCCTCATACTCCTACCAACTGC 2280
 2281 AGGGCACTCGGTCCGGCAGCCAGTCCATCCACCCACACCCAAGTCCCAGCCAGCCGGAC 2340
 2341 CTTACGCAGGACCCCGATGATAGGTGCTTGACGGCTGCAGCAAAAGCCAAGGCCACCTGC 2400
 2401 CGCTGCTGCCCATCCCCGCCAATCTGAGACCCCTAGACTGGACCGCAGAAAAGCGTTTC 2460
 2461 TATGGGAACCCCCCACCAGAAATCACGTGACGCAATCGGACGACCAATCGCTTCTTACC 2520
 2521 TCTGCCCGCGGTCCAGCTTTTGGCCCTCCCTCTCGCCCCCGCCTCCTTCGCCCAGCCCCG 2580
 2581 CCCCTTGCTGCGGAGAGCCCGCGCTGCGCGCTGTGTCTGCGCGCTCCTTCCCTCGCG 2640
 2641 CGCGCTCTCCGTGGAAGAGCAGGGGCAGCGTGGGAGGCGCCAAGGGAGCGCGAACCTGAG 2700
 2701 GAGGAAGAAACGGGGCTAGCGCGCAGGCCAGAACGGTCCGAGCCGCGGCAGTCCGGCGAC 2760
 2761 GCCTCAGAGCGGAAGAGGGGAAGTGAATCAGGCGCCGGGTAGTGGGTTGCTGGGCTGGGCT 2820
 2821 TGCTGAGGTAGAGGCAGCGCCAAGAAGAGGCCTTTGCCGCTGGTCCGGATTGGGATGTCTG 2880
 M S
 2881 AAGAACACAGTGTGCTCGGCCCGCTTCCGGAAGGTGGACGTGGATGAATATGACGAGAAC 2940
 K N T V S S A R F R K V D V D E Y D E N

Fig. 22 (continued; 2/5)

2941 AAGTTCGTGGACGAAGAAGATGGGGGCGACGGCCAGGCCGGGCCGACGAGGGCGAGGTG 3000
 K F V D E E D G G D G 2 A G P D E G E V

3001 GACTCCTGCCTGCGGCAATATCCTTGCATTCAACGGCCCTCCCCACCCCAGCCCAGCCCAG 3060
 D S C L R Q

3061 CCCGCCCTTCTCCTGGGACCCGGGAGCCTGCAGGATCCGCGGGGCACCCGGCGGGAGCTG 3120
 3121 CCTCTCAACCTGCGGCTTAACCTGTCTCTTTGGGATCGCCCGCTCTGAGAGGGCAAGGGG 3180
 3181 GAAGCCCCCGTTTCTACCCAGTCGGCAGGAGACGCGAGGGTCCCCTCTTGGGAAGCCTG 3240
 3241 CCCTACCCCGCGCGCCTTCCACGCCCCCAGATTCCCTCAGGTTGCACCCGAGTGCCTGCCT 3300
 3301 GCCTCGGGAAGTGGTCCCGCGCCCGCGCCCTCGCGGCGCTGGGGAAGGCGGCCCGGCT 3360
 3361 GGTGGGGAAGGCTGGTGCCGACCGCCTTAGTTTTTCTTCTAGAACTCTGATTTCTTGGG 3420
 3421 GTCACATTAGCTCCAGAAATTTCTGATTGTGGGGAACCTGCATCTTTCCTTAGTGGTTTT 3480
 3481 GTTTTTTGGTTGTGTTTTGTTATTGGTAGCGTTAAGGTAGTTTATTGCTTACCGGGGGG 3540
 3541 CCGGGGGAGATGGGACTGTTGAAAATTGAGGTCCTGTGCTTTCAGCCCATTGGCCCTT 3600
 3601 TTTAAAAAAG 3660
 3661 AATTTGTTAACTGGGGGAGGGGAATGAATACAAAAAATAACAACTCCTAGAAGGAAGCT 3720
 3721 TGGAGCCTTTTACCTGCTAAGAAAAGGACAATAGAAAAAACAACGGGGAATGCGTGTGGA 3780
 3781 GAATCCTTGGAATATTTAAAAATAAACCCTTAATAAGATAGAAGATGAGTCATTTCGT 3840
 3841 ATAAAGCAGAATCATTTTTGTAATCCTAAAAATTTTCCATTTTAGTTAAAAATATGGCAG 3900
 3901 TCAGTTCCCGGTTTCTGTTTTTGCATATTTGAATATTCATAACTTTGGCTTCGATTTGC 3960
 3961 ATTACATCTTTTTTAGAAAAATGTAAATGTTGCAAAAAACCGAAGCTGTAGTTTTAGAA 4020
 4021 AATCTCAGACACTGAATTTGTATGCATTTCTAATTCCTGGGTGTATTCATAAGGAAGACT 4080
 4081 CTCAACAATGTCCTGTTATAGTGGGGAATATGAGAGTGAAAATATTTAATGGCAACAAT 4140
 4141 ATCCTTTTTTAAAGGCACCTAAATAGAGCATTAGACATTTATCAATATATAGATAGTGCT 4200
 4201 TTGCCCAACTTTACAAATTAATTAGCTGTTGCTCTTTTGCATTATTTAAATACTTAAGTG 4260
 4261 CTTGGAGTTATAAAAAATGAGCTAATCTACATCAGGCATGCTTCTCTAGAAATCCCTGCA 4320
 4321 GCCTTGAAAATAACAGCTTGTCAACCAGAGATTTTGTGTAAGAACTTTTTCTTTAGAAAA 4380
 4381 TAAATGGTGAACATGCTTCTAAAAACATTATTTGTGATGGGATAAGATGGTGTTTTATG 4440
 4441 AAACCCCAAGTGTATTTTAGGTAATTTGTGGTGACTTTTAAAGGTACTGCTGTATCCATA 4500
 4501 TCAGTGGATCTGCTTTTTGATCAGTTCATCTTAAATATAAAGATACTGTCTCTTCTTAC 4560
 4561 CGTTACATACAGCCAGGAAAGACAGCCCTAGTGGTGGGGTACTAGAGTTGGAGGAACAAG 4620
 4621 TGAAGTCTGTGGTTTTCTTTTAGGGGAATGTTGTACATTCTGACAGTCTGATTTGGCCT 4680
 4681 TCTGTTTCTCATGCTTGTCTAAGTCACTAGTGCTTTCAAAGAGAGCCTGAATTTAATAGGT 4740
 4741 ATGGTCTAACACAGTTTGAATAACCTTTGTGAAATATGAGAGAAAAATATCTAAAGCAAAA 4800
 4801 AATTAAGCTGCCACCTAAGGGACATATGAATATTACATCTTCTGTGATGCCTCTTTTCA 4860
 4861 TCAATATTGAGAGATTGCTAATGTGTATCATTCAGATTGCTAATCTGCCAGCATGTTCTA 4920
 4921 CCAGCATTTTCAGATAATACAGAATATGGTCTAGCAAAAGTTTGGTCTTTATTTTTCAA 4980
 4981 TTAGAATCACAGGAAAAGACATATTTTGGTTGATAATAGGTATTTTCAATTTGGGGGACTA 5040
 5041 ATAATTCTGATATATATTTTAGGATTTCTTTAACACCACTCTAGGTAATGTTTGCATATG 5100
 5101 TATCTCACTGGGAAATGAAAGACTATCAAGGTGTTCACTTGATAGTTAGAACCAAGGGTG 5160
 5161 AAACAGTCTTTGCTTTATTAATAAAAAAGTCTAATGTCTATTTTGCTTTTGATATTTTGC 5220
 5221 CTTTGATTAACATCCTGGAAACCAACACATTGAATTTCCAGTATTGAACATAGTGACCAA 5280
 5281 AGTAATTTTCTTTTTATATGTAAATCAAGTCATAAAGAACCAGTGGTTATAATGCTTTCT 5340

5341 GGGGGCCATCCTTTGCTGTTACACCCTTAACTTCCATCACAGGAAACATGACAGCTGCCC 5400
 G N M T A A L

5401 TACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGTGAGTC 5460
 Q A A L K N P P I N T K S Q A V K

Fig. 22 (continued; 3/5)

5461 GCAGACTACACACAGTGATCTCTGCTGATATCTTATTCTTAGTAAATCCTTGCAGTGC 5520
 5521 AAAAAAAAAATCAATATTTTAACTGTTTGCTATCTTTGACAAGAAGAGTTTATAATGTAGT 5580
 5581 TTGATAGGTAAAAATTTACAGTGAAAAATAGCCCTATAATGTAGTTATGATAATGCTGC 5640
 5641 ATGGTAAGATACAGTAAGTTCAAACGATAGTGAAATCATTGTGTGTGTTTTTAGAGGAG 5700
 5701 ACCACTCAGGCTGAATTTGAGCAAAGGTTTGAATAAAGTTAAACCTTTACAAAAATAA 5760
 5761 ACAGATTGTAATTGCTTTTTTAAAGATTTTTTAAACCATACAAATACTAAATACTTATTA 5820
 5821 TAGAAAGCTCAGACATATGAGAAGGTTAAAAAGATAGTGGTTTGTGGTCCCAGCACCCAG 5880
 5881 AGATAACAGTTACTACTTTGGGGCCTTGCTGTATTGTTACAGAGTTCCCTTTTGTTTTTT 5940
 5941 TAAGAATGAATTTTTTAAACGGGCTTTTTTCAAGCTATATGCAATGGTACATGAGCTTTCCT 6000
 6001 TCCCCAATAAGTTAATAGCCTTTTTTAACTTGTATATGGATAAGCTCCAGTGTATACA 6060
 6061 TAATAATCTTTTGTATATTTAGACTGACTTTTTTTTCTATTGTAAACCACTGAAA 6120
 6121 TCAATATTTTTTGGTAAATTTTAAATGTTCTCTTTGAGTAAATTGCTAGCAGTGAATTA 6180
 6181 CTGGATCAAAGAATGCACCTTTTTTTAAGGCTTTGGTATGCAGTATTGCCAAATTGCC 6240
 6241 TTCAGAACAGTTGTGCACTTACATTCTCTGCAGTCTTTTACTAATTCTTAACCTATTTA 6300
 6301 CGTATTTATTTAAATGATGCCATAGCATCAACCCGTTGTCCATAGCTATTCATACAT 6360
 6361 CCTAGGAGCTTCAAGAATCTCAATTGAATAGTAGTAAGTAATACTTAGGTAATGCATA 6420
 6421 ATAATTATCTAGGTAACATAATTTTTTATGGGGAAATTTCTTTGGTTTTTACAAGTTG 6480
 6481 TAAAGATTGTCGTTGAAATTTCAATTTTACCCTGGATGCAAAGATATTTTCTAAATCTG 6540
 6541 GTAATTGCAGTCTTTAAACCAAGATAACAGTAGGTGGTAGAAACATTCTGTGAAATCCT 6600
 6601 GACCAGTAGGAATGCTGGAGGTATCACTTTGTGTGAATGGAAGGAGAAACGAATTGTTG 6660
 6661 AAAAGGTCAGTTAAGTGTTCCTTTGCTTGGCCGGATGGGTAAGAAAATAACTGCTTTTG 6720
 6721 AAGCAGGCTTTTGCCAAAGAAAAAGATCATTATTAATGAACATCACTATATTTCAATC 6780
 6781 TACAGTCAATTCATATAAATTACAGTCAATTTCTTTAAGACAGCTTGGTTTATTAAAA 6840
 6841 TTTTAAATAAAAAAGTTTTTAAAGAAAAATTACTTCTGAAGGATAATTCAAGGTGAAAC 6900
 6901 TGCAAATCTGCCTCCTTGTTTTGTTGGGAATTTTTTTTTTTTTTTTTTTTGTAGACG 6960
 6961 GAGTCTCACTCTATCACCCAGGTTGGAGTGCAGTGGTGCAATCTCAACTCACTGCACCCT 7020
 7021 CCGCCTCCCGGGTTTAAAGCAATCCTCCTGCTTCAGCCTCCCGAGTAGCTGGGATCACAGG 7080
 7081 CACACACCACCATGCCTGGATAATTTCTGTATTTTGAAGAAAACAGGGTTTACCATT 7140
 7141 TTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCTGCCCATCTCGGCCTCCCAA 7200
 7201 GTGCTGGGATTACAGCTGTGGGCCACCACCCCGCCGTTTGTGGGATTTTTTTTTTTT 7260
 7261 TAAGATCAAGACATAAATTTAAATGTTGTTTTAATAAATTGTTAAATTATCACATTGATC 7320
 7321 TGTTAGCAAACTCTCTCAGCTCTGCCTTCAATTATGTTAATAGTCTGTCAAGTTTCTTAC 7380
 7381 CACCTCCACTGCTACTATGCTTACCACATCCAGCCTGTATTATTGCAATTGCCTCCTAAT 7440
 7441 TGCTCTCCCTGCTTCTACCTTATCCCTACTCCACAGCTTATTTCTGTAAACATAGATG 7500
 7501 CCAAAGCAATCCTGTTAAATGTGAGTCAGATTATGGCACTGCTCTTAAACCTTCCAAT 7560
 7561 GTCTTCTCATTTCTCTCAGTAAAGCCAACTCCTTACAATGCCTGTAGGCCTTACACGA 7620
 7621 TCTGTCTCCATAACCTCTGACTTACTCACGTGCTTTTCTCCCAACCAATCCACTCCAAC 7680
 7681 CACATTGGGTTTTTTTCTGTTCTGGAACACACTGAACACACACTAATAGCACTGTTCTT 7740
 7741 TCCTCTGTCTGAAACACTTTCCTCAGTTATCCCAAGCCTTCTTTCAGTCTTTCAGGTCC 7800
 7801 TTAATAATGTCACATTATAGTGTAGACTTTCTGAAATCTAAACCTCCTCATAACAG 7860

 7861 ATATGTCTAAATGTTCTGTTATTTATTGACCCACCAGGACCGGGCAGGCAGCATTGTCTT 7920
 D R A G S I V L
 7921 GAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAAAAGGCAGTTCAATCTCTGGACAA 7980
 K V L I S F K A N D I E K A V Q S L D K
 7981 GAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCGTCTGACAA 8040
 N G V D L L M K Y I Y K G F E S P S D N
 8041 TAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGTAAGTTATGAATTATAAATCTATAT 8100
 S S A M L L Q W H E K

Fig. 22 (continued; 4/5)

8101	GACTGGTTCTTTTACAATAGGGAATGACAATGACAACCTCTCTCACCTAAATAACCATTT	3160
8161	TGATTTGTTGTACATTTTGTATTACAAATAAAATGCATGAAAAGGATACTTCATATTT	3220
8221	ATGTTTACTAGCCTTGGTCTTAAGAGATTCTGATTCCAACACTTGTGTTTATTCAACAAT	3280
8281	GATTATTAGTAATTAACATAATCTTGAACCTCTGAATTAATCAAAACTTTGTAAAAGAA	3340
8341	AATAAGCAATACAAATCAAGAATCTTTTCACAGTGACCAAAAAGGTGAAACACACACAGG	3400
8401	ATCGAATATGATTCAACCA	3419
8420	TTAAAAGGAATGACATTCTGACACATGCTATAACATTAATAAACCTTGAAACATACCAA	3479
8480	GTGAAATGAGCCAAACACAAAAGAACTAATATTTTATAATTTTACTTATATGAAATAATC	3539
8540	TAGGATAGGCAAACACAAAGGGACAGAAAGTCCTTAGAGGTTACTAGGAAGTAGGGAAAG	3599
8600	CAAGGAATAGGGAGTTAGTGCTTAATAGGTACAGAGTTCTCTCTTGGAGTGGTAAAAAG	3659
8660	TTTTGGAAACAGATAGTGGTGATGGCTACAGTACATTGTGAATATAATTAATGCCAATGG	3719
8720	ATTTTACACTTAAAGATGGTTAAATGGCAAATTTTGTGTTAGATATTTTACAACATTTT	3779
8780	TAAAGAATTAGGAGTTTGGAGGATCAAGAATCTTAAATCATGTTTTTCTATTTTCATGT	3839
8840	GTATATTTTGCAATGTAAGTAGATGCTGGTACATCATCTGTCAAAAGAGTATAAGTGATT	3899
8900	TTGAGCTTTGGGTAAAAAACTGGATAACATGTAAATAGAACCAGTCATAAAATATTGAG	3959
8960	TGTTTGAAGTGTATCTGAGTGAACACACAAACATAAGAAAAAGCACATAGTAAACAAT	4019
9020	AGTTCCCCCTTTTACTCTAAATGCACCAATTTGGGTAGTAATTTATATGGCACCCCTATT	4079
9080	CATGGAACACTTTCTGTTGCCAGGTACCATACTATTAATGTTTTATTTAACCTTTACAAC	4139
9140	AACCCTGTGGAAGTATATAAATATCTTTATCATCCTCAATTTACAGATGAAAAGCTAGCT	4199
9200	TTAAAACCCCAAGCCAGCGTAGTTCTAGCATAGCCTCAAGATTGCAGTGAACATTGATTAC	4259
9260	TTATTATATTCCACATATTCTTCAAAGGACTTTATAAATATTAACCTCATTTAATCCTCAT	4319
9320	AAAAATGGAGGGAAATGCTTGCTATTATCTCTTTTGTCACTGAGGAACTGAGGCATG	4379
9380	TGTGAAGTCTTCATTTCTTCCAAATGTCAGTCACCAAGTTTTTACCAATCTTCGAAGTATT	4439
9440	TCTGAAATCTATCTGTTCAAGCGTATCTAATGCAGCTGTTACAGCATCTCTCCAGTCT	4499
9500	GTTGCCATAGCTTCTCTGACTGGTTTCCCAGTTAAACAGTTTTTGCCCTCCTTCAAATCTGTT	4559
9560	TCCACCCAGCCATCAAATGATATCTTTAAATCAAAATTGCCCTTGTCAGTCACCTGCA	4619
9620	GGGATAAAGTCAAAGTTCCTCAAGTCTAGCTTCATCTCCATGTCATTCTTCCCCCTCAGGC	4679
9680	TATAGCAATGCCAGCCTTTTCTGAATGCACCATATTGTTTCACACCTCCATACATTTG	4739
9740	CTCATGATTTTCTGGTGTAGCCTGTACCTACTCATTCTTTAATGTGTCAATTCCTCC	4799
9800	ATGAAGCCTTAGCTGAAACATTCCTCTATACTGTTAATCTGGGTATAAGCCTCTCCCTGG	4859
9860	TGCTTTAATAGCACCTGCAGCACAACTCTCATTTATACATTAGATTAAATTACCTGTT	4919
9920	TATATGTCTGTCTCCTCATGCTAGACCAGAAAATGCTGTATTTGTTCACTTTTGTATCCC	4979
9980	CAGCATCTAGCACAGTACTCAGTATACAAAAGGTATTCCATAAATATTTTTTGAACAGAAA	10039
10040	GAAACCAGAGCTCAGATTCTTAATACTTGATCATTACTCTCTATTTTTTCAAATTAGAGTC	10099
10100	AGAGTTAAAGTTTCTAAGTTCTTAGCTATTAACAATACCTTCTTTCTTTGGGAGAAAAA	10159
10160	AAATCTGACAAAGGCTGACTAATCGAAGTGGAAGTTGGGATGGTTGATCCAGTTTGAAT	10219
10220	TTTCTTCTGACTATGTGGTGAGAATGAGAAATGCAGAATGTCCACCTGTTTTGAGCAGGA	10279
10280	ACACTATGCTGCAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGAGACGGAGTCTTGC	10339
10340	TCTGTGCGCCAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCCTCCT	10399
10400	GGGTTACACCATTTGTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCCA	10459
10460	CCACGCCCCGGCTAATTTTTTGTATTTTTTAGTAGAGACGGGGTTTTACCATTGTTAGCCAGG	10519
10520	ATGGTCTTGATCTCCTGACCTCGTGATCCGCCGGCCTCGGCCTCCCAAAGTGCTGGGATT	10579
10580	ACAGGCGTGAGCCACCGCGCCCGGCTATGCTGCAGATTTTTTAAACATTATTTAGAAT	10639
10640	TAATGTACTAAATGTAACTAGTATCTCACTAGAATGTAACCTTCATGAGGGCAGGGACT	10699
10700	TTCAAGGTTTTGTTTATTACTGTAACCTCAGTGCCAAGAACAGTACCTGGTGCATAATTG	10759
10760	GTGCTCAAGAATTTATTATTTGTTAACTAATAAATTCAGGGTCTATAGCAGTGCCCATTC	10819
10820	CTTCTTTAAGAAAAATGTTTTACCAAATATGAGAATTGACCTTTTATTATTCTGTCAACA	10879
10880	TTTACATCCTGGTTTTGTTTTTAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTTCTGTG	10939
	A L A A G G V G S I V R V	
10940	TCTTGACTGCAAGAAAACTGTGTAGTCTGGCAGGAAGTGGATTATCTGCCTCGGGAGTG	10999
	L T A R K T V *	

Fig. 22 (continued; 5/5)

11000	GGAATTGCTGGTACAAAGACCAAAACAACCAAATGCCACCGCTGCCCTGTGGGTTAGCATC	11059
11060	TGTTTCTCTCAGCTTTGCCTTCTTGCTTTTTTCATATCTGTAAAGAAAAAATTACATATC	11119
11120	AGTTGTCTCTTAATGAAAATTGGGATAATATAGAAGAAATGTGTTAAAAATAGAAGTGTT	11179
11180	TCATCCTTTCAAACCATTTTCAGTGATGTTTATACCAATCTGTATATAGTATAATTTACA	11239
11240	TTCAAGTTTAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTGTTCTGTTTTGTTT	11299
11300	TGTATTATTTTTAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCT	11359
11360	CATTGCTAGTCAGGGAAATGATATTTATAAAAAATATGAGAGACTGGCAGCTATTAACAT	11419
11420	TGCAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATATGTTTTTGGAAATAAGTGG	11479
11480	TGGGTGAATACCACTGCTAAGTTATAGCTTTGTTTTTGCTTGCCCTCCTGATTATCTGTAC	11539
11540	TGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCCCTCAATTTATT	11599
11600	TGTGGTCACCCAGGGTTTCAGAGCAAGAAGTCTTGCTTTATACAAATGTATCCATAAAATA	11659
11660	TCAGAGCTTGTTGGGCATGAACATCAAACCTTTGTTCCTACTAATATGGCTCTGTTTGGAA	11719
11720	AAACTGCAAATCAGAAAGAATGATTTGCAGAAAGAAAAAACTATGGTGTAATTTAA	11779
11780	ACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTTAGA	11839
11840	CATTATGAGGTATACAACCTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTC	11899
11900	AGTGTTCTTCAGGGTAGTTGGGATCTCAAAAGATTTGGTTTCAGATCCAAACAAATACACA	11959
11960	TTCTGTGTTTTAGCTCAGTGTTTTCTAAAAAAGAACTGCCACACAGCAAAAAATTGTT	12019
12020	TACTTTGTTGGACAAACCAAATCAGTTCTCAAAAAATGACCGGTGCTTATAAAAAAGTTAT	12079
12080	AAATATCGAGTAGCTCTAAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCTTAG	12139
12140	TATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATT	12199
12200	CTATAAACTCTTTGCTGTTTTTGATACCTGCTTTTGTTCATTTTGTGTTTTGTAA	12259
12260	AAATGATAAACTTCAGAAAATAAAATGTCAGTGTTGAATAATTTATTTTCTCTGACAC	12319
12320	TTTAACAATTATGAATGTATGGTTAATTAAGAGGAAAGGTTTTCTGCTTCTACCACCAAG	12379
12380	TACTGTACTCTTAACAAGAACAGTTTGGTAGGGTTTTTATAAGACTATATAGATATAAGA	12439
12440	TGATAGAGAAGAGAGTCATGAATGATGTCAGAGCACTACTGAAGCCTTTGGAGTGATTCC	12499
12500	ATAGCCTTCTGGATGGCAGCTGAATACCTATATGTAGTATCACTGCCCAAAGACCTAGAC	12559
12560	TAGAAAGTGCAAAGTAGCTTAGCAGCTGCAGTCATTCACCTCCAGCCTCCAAAATTCTCT	12619

11000 11060 11120 11180 11240 11300 11360 11420 11480 11540 11600 11660 11720 11780 11840 11900 11960 12020 12080 12140 12200 12260 12320 12380 12440 12500 12560

Fig. 23 (1/6)

1 - GATCCCTCTCCAGGTGGAAG - 60 /|\
 61 - CTCCTTCATACCAAAGTTTAAAGGCCCTGGGGATACGAGTAACCTTTGACGACTATGAGG - 120 |
 121 - AAGAAGAAATCCGGGTCTCCATCAATGAGAAGTGTGGCAAGGAGTTTTCTGAGTTTATAGG - 180 |
 181 - GGCATGCCTGTGCCCCCATGGGTTTTCTTTTTCTTTTTCTTTTTTTGGTCGGGGGGG - 240 |
 241 - TGGGAGGGTTGGATTGAACAGCCAGAGGGGCCAGAGTTCCTTGCATCTAATTTCACCCC - 300 |
 301 - CACCCACCCCTCCAGGGTTAGGGGGAGCAGGAAGCCCAGATAATCAGAGGGACAGAAACA - 360 |
 361 - CCAGCTGCTCCCCCTCATCCCCTTCACCCCTCCTGCCCCCTCTCCCACTTTTCCCTTCCTC - 420 |
 421 - TTTCCCCACAGCCCCCAGCCCCCTCAGCCCTCCCAGCCCACTTCTGCCTGTTTTAAACGA - 480 |
 481 - GTTCTCAACTCCAGTCAGACCAGGTCTTGCTGGTGTATCCAGGGACAGGGTATGGAAAG - 540 |
 541 - AGGGGCTCACGCTTAACTCCAGCCCCCACCCACACCCCATCCACCCAACCACAGGCC - 600 |
 Human cAMP-dependent protein kinase
 catalytic subunit alpha
 Accession number X07767 (until *)
 - follow arrow until line that
 begins 1561 -
 601 - CACTTGCTAAGGGCAAATGAACGAAGCGCCAACCTTCCTTTTCGGAGTAATCCTGCCTGGG - 660 |
 661 - AAGGAGAGATTTTATGTGACATGTTCAAGTGGGTGCTTGTAGTAATTTTTTAAAAAAC - 720 |
 721 - AACAAATTTAAATCTTATTTAAGTTCACCAAGTGCCTCCCTCCCTCCTTCTACTCCC - 780 |
 781 - ACCCTCCCATGTCCCCCATTCCTCAAATCCATTTTAAAGAGAAGCAGACTGACTTTGG - 840 |
 841 - AAAGGGAGGCGCTGGGGTTTGAACCTCCCGCTGCTAATCTCCCTGGGCCCCCTCCCGG - 900 |
 901 - GGAATCCTCTCTGCCAATCCTGCGAGGGTCTAGGCCCTTTAGGAAGCCTCCGCTCTCTT - 960 |
 961 - TTTCCCCAACAGACCTGTCTTACCCCTTGGGCTTTGAAAGCCAGACAAAGCAGCTGCCCC - 1020 |
 1021 - TCTCCCTGCCAAAGAGGAGTCATCCCCAAAAAGACAGAGGGGGAGCCCCAAGCCCAAGT - 1080 |
 1081 - CTTTCTCCAGCAGCGTTTCCCCCAACTCCTTAATTTTATTCTCCGCTAGATTTTAAC - 1140 |
 1141 - GTCCAGCCTTCCCTCAGCTGAGTGGGGAGGGCATCCCTGCAAAAGGGAACAGAAGAGGCC - 1200 |
 1201 - AAGTCCCCCAAGCCACGGCCCGGGGTTCAGGCTAGAGCTGCTGGGGAGGGGCTGCCTG - 1260 |
 1261 - TTTTACTCACCCACCAGCTTCGCGCTCCCCCATCCTGGGCGCCCCCTCCTCCAGCTTAGCT - 1320 |
 1321 - GTCAGCTGTCCATCACCTCTCCCCCACTTTCTCATTTGTGCTTTTTTCTCTCGTAATAGA - 1380 |
 1381 - AAAGTGGGGAGCCGCTGGGGAGCCACCCCATTCATCCCGTATTTCCCCCTCTCATAACT - 1440 |
 1441 - TCTCCCCATCCCAGGAGGAGTTCTCAGGCCTGGGGTGGGGCCCCGGGTGGGTGCGGGGC - 1500 |
 1501 - GATTCAACCTGTGTGCTGCGAAGGACGAGACTTCCTCTTGAACAGTGTGCTGTTGTAAC - 1560 |
 1561 - ATATTTGAAAACTATTACCAATAAAGTTTGTGTT*TAAGAAAAAGTGTGCTGGTGTCTC - 1620 |
 1621 - GACTTCGATCACCCACCCACACACCCCGGGGTTTGGAAAGGGAATTTTCGGACCCCAGC - 1680 |
 1681 - GTGCAGGCCGATCAGGTCCTGGCTTGAAGTCCTTGTAACAGGGTTTAGCTGAAATTCG - 1740 |
 1741 - GCACTCCTTCGGCCCCGCGAGGAGAAACGAGCGTCAAACCTGCCCTTTGACCCAGATTCCG - 1800 |
 1801 - GGTCCCCAATCTGCGGCGCGCCCCCTCGGCGTCCAGCCCGGACCGAGAGGGCGCTCTA - 1860 |
 1861 - GGGAGGCGCTGGGGCTGGCGCGCCAGGAGGCCGAGCGGCGGGGGCGGCCCTGGCAGG - 1920 |
 1921 - GGGAGTAGAAGGGGGAGAGGGTGGCGGCCCCCTTCCCGCATCCTCAGCGCCGGGCCAGG - 1980 |
 1981 - CGCGCCTGAGGGACGCGGGGGCGGCGGCAGGAGGGTCCCGCAGCACCTGCGAGCG - 2040 |
 2041 - CGGCAGCCCCGGCCCGGGCGGCGGAGTTCCCGGTAAGTGCCTGTCGAGAGCGGAGCGC - 2100 |
 2101 - GCTGGAGAGGCGTGGAGAGGGGGGCTGGGCGCCGGGACGTCTGGGTCCCGCGCCCAATG - 2160 |
 2161 - GCTGGAGGGCGGCGGAGCGCCGCGCCCGCCCTGCCCGCCCCCTCTCCCCCTCCCCCGG - 2220 |
 2221 - CACTCCCTCCCCCTCCCCCGCCCGCGCTTTCCCCCGCCCCCGCCCGGCCAACTCC - 2280 |
 2281 - GCGGCGCTCCTTAAAAAGCGCGCGGGAGTTGTAAGGGGGGGCCGGAGCGAGCCGGAGTG - 2340 |
 2341 - AGCGAGAGCGCAGGGTAAAGGGGGCGGGCGGGGGGCCGGGCTCCACCTTAAAGCGGGC - 2400 |
 2401 - GCGTGGGGGTGGGAGGGAGGAAGGCGGGCGGGGAGGAGGGAGGGAGGGAAGGAAGGG - 2460 |
 2461 - GGGCCGGAGTGTCCCGGGCGCAGGGCGCGCTGCGGCGGCGGCGGCGGGGAGGGGCC - 2520 |
 2521 - GGCGCGCGCGCTCCCCCTCCTCCCCCTCGCATCCCCGGCCCCGCGCGCCCCAGAA - 2580 |
 2581 - GCGGGTCTGTGTGTGCGTGCAGTGCAGTGCAGTGTGTCATATTTTTTCTCTCTTT - 2640 |
 2641 - TCTTTCTCTCTACTGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTTT - 2700 |
 2701 - TTTTTTTTTTGCAGAAAGAACAGCAGCGCCGCGCGCTCCGCGAGGCGCTGCGCCCCC - 2760 |
 2761 - GGGGGGGAGGCGGAGGAGCGGGCAGCGGCGAGGGAGGGGAGCCGGGAGGGGGGCGC - 2820 |

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Health	0.8	0.4	0	1
Smoking	0.3	0.5	0	1
Alcohol	0.2	0.4	0	1
Exercise	0.6	0.5	0	1
Stress	0.7	0.5	0	1
Sleep	0.8	0.4	0	1
Work	0.9	0.3	0	1
Family	0.7	0.5	0	1
Friends	0.6	0.5	0	1
Community	0.5	0.5	0	1
Religion	0.4	0.5	0	1
Politics	0.3	0.5	0	1
Art	0.2	0.4	0	1
Music	0.3	0.5	0	1
Reading	0.4	0.5	0	1
Travel	0.5	0.5	0	1
Volunteering	0.6	0.5	0	1
Philosophy	0.7	0.5	0	1
Science	0.8	0.4	0	1
History	0.9	0.3	0	1
Geography	0.8	0.4	0	1
Language	0.7	0.5	0	1
Mathematics	0.6	0.5	0	1
Physics	0.5	0.5	0	1
Chemistry	0.4	0.5	0	1
Biology	0.3	0.5	0	1
Medicine	0.2	0.4	0	1
Law	0.1	0.3	0	1
Business	0.2	0.4	0	1
Engineering	0.3	0.5	0	1
Architecture	0.4	0.5	0	1
Design	0.5	0.5	0	1
Writing	0.6	0.5	0	1
Acting	0.7	0.5	0	1
Dancing	0.8	0.4	0	1
Sports	0.9	0.3	0	1
Gardening	0.8	0.4	0	1
Cooking	0.7	0.5	0	1
Crafting	0.6	0.5	0	1
Fishing	0.5	0.5	0	1
Hunting	0.4	0.5	0	1
Collecting	0.3	0.5	0	1
Traveling	0.2	0.4	0	1
Volunteering	0.1	0.3	0	1

2821 - CGCGCTGGGAGGGAGGCAGCGCGCACGGTGCAGCCGGGCCCGGGAGGCATGGCGGGG - 2880
- M A G

2881 - CCCCCGGCCCTACCCCCGCCGGAGACGGCGGGCGGCCGCCACCACGGGCGGCCGCCCTCG - 2940
- P P A L P P P E T A A A A T T A A A A S

2941 - TCGTCCGCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGACTCGCTGCGC - 3000
- S S A A S P H Y Q E W I L D T I D S L R

3001 - TCGCGCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGGGCGGCACGGC - 3060
- S R K A R P D L E R I C R M V R R R H G

3061 - CCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAACTGATCCAGCAGCGCGCCGTGCTC - 3120
- P E P E R T R A E L E K L I Q Q R A V L

3121 - CGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGCGTCCAGCCGCCCGG - 3180
- R V S Y K G S I S Y R N A A R V Q P P R

3181 - CGCGGAGCCACCCCGCCGGCCCCCGCGCGCGCCCCCGCGGGGCCCCCGCCGCCCGCC - 3240
- R G A T P P A P P R A P R G A P A A A A

3241 - GCCGCCGCGCCGCCGCCACGCCCCGCCCGCGCCACCGCCCGCGCCGTGCGCCCGCC - 3300
- A A A P P P T P A P P P P P A P V A A A

3301 - GCCCCGGCCCCGGCGCCCCGCGCGGCCCGCGCCGCCACAGCGCCCCCTCGCCTGGC - 3360
- A P A R A P R A A A A A A T A P P S P G

3361 - CCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCCTGGCCGCGCCGCCGCCCG - 3420
- P A Q P G P R A Q R A A P L A A P P P A

3421 - CCAGCCGCTCCCCCGGCGGTGGCGCCCCCGGCCCGGCCCGCGCCGCGCCCCCGCCGCC - 3480
- P A A P P A V A P P A G P R R A P P P A

3481 - GTCGCCGCCCGGGAGCCGCCGCTGCCGCCGCCGCCACAGCCCGCGCGCCGCCACAGCAG - 3540
- V A A R E P P L P P P P Q P P A P P Q Q

3541 - CAGCAGCCGCCGCCGCCAGCCACAGCCGCCCGGAGGGGGCGCGGTGCGGGCCGGC - 3600
- Q Q P P P P Q P Q P P P E G G A V R A G

3601 - GGCGCGGCGCGGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGCAGCGCGGC - 3660
- G A A R P V S L R E V V R Y L G G S G G

3661 - GCCGGCGGTGCGCTAACCCGCGGCCCGGTGCAGGGGCTGCTGGAGGAGGAGGCGGCGGT - 3720
- A G G R L T R G R V Q G L L E E E A A A

3721 - CGAGGCCGTCTGGAGCGCACCCGTCTCGGAGCGCTTGCCTGCCCCGCGGGGACAGGCC - 3780
- R G R L E R T R L G A L A L P R G D R P

3781 - GGACGGGCGCCGCCCGGCCAGCGCCCGCCGTCTCGCAGCAAGGTGAGCGCGCCGGGG - 3840
- G R A P P A A S A R P S R S K

3841 - AGCGGGGGCGCCGCGCGGTGGGCAGGTGCGGGCGAAGTTGGTGGCGGGGGCGCGAGTCCC - 3900
3901 - GGGAGGAACTGGGTGGCGGGTGGCTGGGGCTTTGCGCGCGTTTCTGCGGGCTCGGTGCG - 3960

Variable	Mean	SD	Min	Max
Age	34.5	10.2	22	55
Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	1.5	9	16
Income	15.2	3.5	10	25
Health status	1.8	0.6	1	3
Stress level	2.5	0.8	1	4
Life satisfaction	3.2	0.9	1	5
Work engagement	2.8	0.7	1	4
Organizational commitment	3.5	0.8	1	5
Job satisfaction	3.8	0.9	1	5
Turnover intention	1.5	0.6	1	3
Organizational citizenship behavior	2.2	0.7	1	4
Employee well-being	3.0	0.8	1	5
Work-life balance	2.5	0.7	1	4
Job design	2.0	0.6	1	3
Supervisor support	3.0	0.8	1	5
Peer support	2.8	0.7	1	4
Organizational culture	3.5	0.9	1	5
Leadership style	2.5	0.8	1	4
Employee engagement	3.2	0.9	1	5
Job autonomy	2.0	0.6	1	3
Job security	3.0	0.8	1	5
Job stability	3.5	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8	1	5
Job involvement	3.2	0.9	1	5
Job satisfaction	3.8	0.9	1	5
Job commitment	3.5	0.8		

3961 - TGGTGACCTTGGCAAGTGATTGAACTCTCCCGAGCCTCAGTTTCCTCCGCTGTAAACGCG - 4020
4021 - GTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGATTGCGTTGTC - 4080
4081 - GAGGGCTTTAGTTAAACACAGAGCCTGGCACGGAGTGAATGCGTAAAAGTTAGTCCGTATT - 4140
4141 - GTTCTTAAAGGTGGAATCGGTTCTCTCTCCCCACCGCCCGGACGCCACAGTCAGGGTCTG - 4200

4201 - GGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCTCTCGGCTCCAGAGAGGTGGAGAAG - 4260
- R G G E E

4261 - AGCGAGTACTTGAGAAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATG - 4320
- R V L E K E E E E D D D E D E D E E D D

4321 - ATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCTCTGCAGGTGCCCAGCACCACC - 4380
- V S E G S E V P E S D R P A G A Q H H Q

4381 - AGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCT - 4440
- L N G E R G P Q S A K E R V K E W T P C

4441 - GCGGACCGCACCCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGGCAGCGGCACCCGCC - 4500
- G P H Q G Q D E G R G P A P G S G T R Q

1 - AGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGGTAAGGATCCCTCTGGGT - 60
- V F S M A A M N K E G G T

61 - GGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCCAAGACAAAGCCAAAGACAGGTGTTT - 120

121 - TTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCGTGCCTTTGCCC - 180
- A S V A T G P D S P S P V P L P

181 - CCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCTTTGGCTGTCCGTAAGTTGGG - 240
- P G K P A L P G A D G T P F G C P

241 - GTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTGGTACAGCCAGAGAGACATCCGTGTT - 300

301 - CACTGGTGTCTGTTTGTGTTTGTATGCAGTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGT - 360
- P G R K E K P S D P V

361 - CGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGC - 420
- E W T V M D V V E Y F T E A G F P E Q A

421 - GACAGCTTTCCAAGAGCAGGTGAGTTTCCAGCCCAGGACTACACACTGACAGACACAGAG - 480
- T A F Q E Q

481 - GGCCTCCCTGGGATGTGCCCTGATCCCGGCTTTCTCTGTTCTGTCCACCCAGGAAATT - 540
- E I

541 - GATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC - 600
- D G K S L L L M Q R T D V L T G L S I R

601 - CTCGGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTT - 660
- L G P A L K I Y E H H I K V L Q Q G H F

Fig. 23 (continued; 4/6)

661 - GAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCGCCAGCCTCACCCCTGCCCCAGCC - 720
 - E D D D P D G F L G *

721 - CATTCCGGCCCCCATCTCACCCAAGATCCCCAGAGTCCAGGAGCTGGACGGGGACACCC - 780
 781 - TCAGCCCTCATAACAGATTCCAAGGAGAGGGCACCCTCTTGTCCTTATCTTTGCCCTTG - 840
 841 - TGTCTGTCTCACACACATCTGCTCCTCAGCACGTGGTGTGGGGAGGGGATTGCTCCTTA - 900
 901 - AACCCAGGTGGCTGACCCTCCCCACCCAGTCCAGGACATTTTAGGAAAAAAAAAATGAA - 960
 961 - ATGTGGGGGGCTTCTCATCTCCCCAAGATCCTCTTCCGTTAGCCAGATGTTTCTGTAT - 1020
 1021 - AAATGTTTGGATCTGCCTGTTTATTTTGGTGGGTGGTCTTTCCTCCCTCCCTACCAACC - 1080
 1081 - ATGCCCCCCTTCTCAGTCTGCCCCCTGGCCTCCAGCCCTAGGGGACTAGCTGGGTGGGG - 1140
 1141 - TTCCTCGGGCCTTTTCTCTCCTCCCTTTTTCTTTCTGTTGATTGTGCTCCAGCTGGCTG - 1200
 1201 - TATTGCTTTTTAATATTGCACCGAAGGTTTTTAAATAAAATTTTAAAAAAGAAAAAGG - 1260
 1261 - GAAAAAAGCCACGGAGTCCATTTTATGAATGGGGTGGGGAGAGGGCACTAAAGAGCCT - 1320
 1321 - CCTAAGAGAGCCTCAGGTTAGGACAGAATTGTTTGGGGAGGGAGAAAAACAGAAACAATG - 1380
 1381 - AATTATAGCTGCCTCACAGCCATGTATAACAATAATTGCTCCAGGAAGGTGGGAATATT - 1440
 1441 - GCTTTTTTTCTTCTGTAATCTCACCGTGTCCGTGTCCAGAACAGAGCTAGGCACACAGC - 1500
 1501 - AGGTGCTCAATTTTGTTTTTCGTTTAGACAGGTTTCATTCTTTCACCCAGGCTGGAGTG - 1560
 1561 - CAGTGGTGCTATCATAGCTCATTGTAGCCTCAAACCTCTGGGCTGAAGTGATCCTCCAC - 1620
 1621 - CTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCACCTGCCATGCCGGGCTAACTTTTAA - 1680
 1681 - AAATTTTTGTCCGGGCACAGTGGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG - 1740
 1741 - TGGGTGGATCATGAGGTCAGGAGTTCAAGATCAGCCTGGCCAAGATGATGAAACCTGTG - 1800
 1801 - TCTACTAAAAATATAAAAAAAATTAGCTGGGCGTGGTGGTGGTGCCTGTAATCCTAGC - 1860
 1861 - TATTCAGGAGGCTGAGGCAGAGGATTGCTTACACCTGGGAGGCGGAGGGTGCAGTGAGCC - 1920
 1921 - AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCTGTCTCAAAAAAAA - 1980
 1981 - TCTTTGTGTGTGTGTGGAGATGAGGGTATGCACTTTGTTGGCCAGGTGGCCTCGAACTC - 2040
 2041 - CCAGCCAAGCAATTCTGCCTGGGATTACAAGCGTGAGCCACCATGCCTGGCCTCAAATAT - 2100
 2101 - TGTTGAATGGCTAGCAGTTAAGTCCTTGGGTTTATAAGCATTTCTCAACTGTCCTCCCA - 2160
 2161 - AGTCCCCATAAGACAAAAAACTCATAAAATCCCACCTTACAGAAGAGGCAGCTGGCCCCG - 2220
 2221 - CACAGAGATGCTGTCTGCCCCGGGTACACAGGGTGGCATCTGACACCCTGTCTGAGTTC - 2280
 2281 - TTCACTCAGAGTCTTTAAATATAATTAGCGTATTTGACATAATGTACATTA AAAACTATA - 2340
 2341 - AACCTGTCAGCCTTTGTCTACTGCAAAGAATCCACTACAAATATTGGGGCAGGGATCTGT - 2400
 2401 - TCTTGGACCATAGTAGTGTCTCCAGACCTCATGGTCCTCTTCATTAAACAACAGAAAA - 2460
 2461 - TCCTTCTGGGCCATCAGATGAGACCATGAGATAGAAGATTTCCAAGTGAAGATTTTGT - 2520
 2521 - CAAGACAGAGTCTTGCTCTGTCACTCAGGCTAGAGTGTACTGGTGCAATCATAACTGTG - 2580
 2581 - TGACAGCCTCGAACTTTTGGGTACAAGTGATTCTCATGCCTCAGACAACACCCAACTAA - 2640
 2641 - ATTTTGGTTTTTGTATAGACAGGCTCTTGCTATGTGGCTTAGGCTGGTCTTGAACCTCTG - 2700
 2701 - GCCTCAAGCAGTCCCTCCCGCTTACGCCTTCTAAAGTGTCAGGATTACAGACATGAGCCAC - 2760
 2761 - CAAGTCCAGCCTGAAGATTTTTAAAAATATTGTTAGTAGTAGTCGCCAGAGTTACTACA - 2820
 2821 - TCCAAAGTCCCTACTAAGTTCTAAGTAGTCCCTACTAAGTTCTAAGGCAGTTTCTCAACT - 2880
 2881 - CATTAGAGTTGTTTTTTGTTTTTAAAGAAAAAAGAGGCTGGGCACTTTAGGAGACCGAC - 2940
 2941 - ACGGGAGGATCGCTTGAGTCCAGGAGTTTGAAGCAACCTGGGCAACATGGGCCCCCATC - 3000
 3001 - TCTAAAAATTTTAAATTA AAAAATGTTTTAACAACAAAAAGCGTTCTGGGAGTGAGGGG - 3060
 3061 - CTGGGGCCTGGGCGGCCTCATTCATATACCTGTGCCGGGTGAGGGGTTGGAGACACGT - 3120
 3121 - TTAGAGACCCCTCCACTCTAGGAATCCACCTCGAGAGATAAAGGTCCCGGCCCTAGCCAC - 3180
 3181 - ACCCCCAGGACACGGCCAGAGGCCACCTCCCTAGGCGGGTCCCTCCCCACCGCCAGGTT - 3240
 3241 - CTGGAGCGCGTGCGGGCGGTGTGCAGGGGTAGGGGGCCGAGGCGCGCGGACTGGAGAGG - 3300
 3301 - CGCGCCCCCTCCCGCGTGTGAAATTCAAAAAGAGGCGAACGGCCCCCGGCGCGGCGCGG - 3360
 3361 - GCTCCGGTGGAGAGGTCAAGGCAGGGGCCAGTCCGAGGCTCCCGGGGCGGGGTGCAACCC - 3420
 3421 - GCGGCCAACCTGAGCAGCAGCGGAAGCTTAAAGAGCTCAGGTTCCCGCCCCCGGCCCTA - 3480
 3481 - CCATGGCTACAGAGCAGTGGTTCGAGGGGTGCTCCCCCTGGACCCTGGAGAAACACCGC - 3540
 3541 - CTCCAGACGCCTTGAACCTGGGACGCCGCCCTGCGGAGACCCCTCCAGGTCGACGCCCC - 3600
 3601 - CTGGCAGGCCTGGGAACCATCTGAGCCGATCCTGAAGATGCCGAGGGGCGGCTGGCTG - 3660
 3661 - AGGCCCCGGGCCTCCACGTCTTCCCCCAAACCTCTGGTCCCCCGGCCTGGGCCAGCACCTC - 3720

Fig. 23 (continued; 5/6)

3721 - CCCGCCTATCCCTGGACACTTTGTTTCAGCCCCATCACCCAAACAGCTGCGCTACCTACTGA - 3780
 3781 - AGAAGGCAGATGATTTCCAGAGCTACTTGCTCTACAGGTGATGCTGGACAGGGTCCCAGG - 3840
 3841 - TCCCCATGGGTAAAGGAGACTTGGAGGGGAGGCGACAGGATGGGTGACACACACCAGGGTC - 3900
 3901 - GCAAAATTACAAGCGCTAGGAGCCAGAGGGAGACAGTGGAGAAGCTAGCATATTAGAAT - 3960
 3961 - CCAGTTTAAAGAGAATGAGGAAGACTGTAGAATTGCGGGTAGGGGATGGCTGCTATTACTG - 4020
 4021 - TCGTGGCAGGGTGGGCCTGGGGTTGTCAAGTCTCTAGGACTTTTCTCCCAGTTTTTAAG - 4080
 4081 - TGCTGTCTTACATTTTGTAGCCCTGTGCTGGCTAAACAAGACCCACCTGAGCCAAACTTGG - 4140
 4141 - CCTGCAGGACATCAGTTTGTAGACTCCAAAGGATAATGTGATTCCCAGACCAGGTTTCCCT - 4200
 4201 - GTGACTCTCAATTTTCAGTGTCCATTGGAATTTCTAGGAGGCTGGGTTGGGTTTGTTC - 4260
 4261 - GTGTTTGTTTTTGTAGATGGAGTCTCACTCTGTGCGCCAGGCTGGAGTGCAGTGGTGCAAT - 4320
 4321 - CTCAGCTCACTGCAACCTCCGCCTCCCGGATTGAAGCAATTCTCTGCCTCAGCCTCCCGA - 4380
 4381 - GTAGCTGGGATTACAGGCGCCACCAACATGTGTTGCCCGGCTAATTTTTTCTTTTCTT - 4440
 4441 - AGTAGAGACAGAGTTTACCATCTTGGCCAGACTGGTCTTGAGCTCCTGACCTCATGATC - 4500
 4501 - CACCCGCCTTGGCCTCCCAAAGTGTGGAATTACAGACGTGAGCCACCGCGCCTACCCGA - 4560
 4561 - GGTGGGTTTTTTTTGTTTTGTTTTGTTTGTATGTGTTTTTTGAAATGGAGTCTTGCTCT - 4620
 4621 - GTCACCTAGGCTGGAGTGCAGTGGGGCGAAGTCACTGCAACCTCCGCCTCCCAGG - 4680
 4681 - TTCGAGGATTCTCATGAGGCTGTTTTTTTTTTTAAATGAGACAGGGTCTCGCTCTGTC - 4740
 4741 - ACCCAAGCTGGAGTGAAGTGGGGCAGTCAAGTCACTGCACCCTCGAACTCCTGGTCT - 4800
 4801 - CAAGCAATCTTCCACCTCCCCTCCTGGGTAAGTGGGACTACAGGTGCCACCATGCCAGC - 4860
 4861 - TAATTATTTTTGTGTAGAGATGGGTCTTGCTATGTTGCCTAGGCTTGTCTGGAACCTCT - 4920
 4921 - GGCCTCAAGCAATCCTCCAGCCTCAGCCTCCCAAACTCTAGGATTGCAGGCGTGAGCCA - 4980
 4981 - CTGTGCCAGACCCTGCAGGAAGCTCTGGGTCTAAGTGTGTGACACTCAGGTGTCAGC - 5040
 5041 - ACTTTAACAAGTGTTCAAATGGGTTTGATGCAGGTAAACCAGAAAGATGTTCAAGAAAG - 5100
 5101 - ACCTGAAACTGGGGGCTTTTCTAATGGGTCAAAGCCAGGGATACAGGTGGGATTGAGTA - 5160
 5161 - GAATGGGGAAACTGCGGGGTGGGGAGGGGTGTGAGGGATTCCAGGCAAAGGCCCCCTT - 5220
 5221 - CTTCTTTCAGCAGAGACCAAGTACAGAAGGAGCAGCTGGCCAAGGCCATGCCACCTTCT - 5280
 5281 - TACAGATGTGTGAGCCCTACTTCTGTACCTGGAGGCAGCCGCGAGAAGCATACCCCCCA - 5340
 5341 - TCTATGGACCCCTGCAGGAGCTGGTCCGAAAGGGGGTGTGTGGAGGTTTCTTAGACCCCA - 5400
 5401 - CGCCCCCTTCTTCTCGCAGCTCTGAGCCTGTGGGGATGGTGGAGGGGGAGGCCCCACTCT - 5460
 5461 - CGCAGGCCAGCTGATCTCACTGTACCCCCCTCTTGATGCAGCTGTTAGAGATCTCCCAA - 5520
 5521 - CAGCTGACCCTGCGCCTGGAACAGCTGGTCCCTCATGTACGCTTCTTTGGGTTCGTGGAC - 5580
 5581 - CTGGAGGAGATGAACCCCTTAGGTAAATGGTAGGAGACTCAGATGGGGGGATGAAGGA - 5640
 5641 - GTCCAAGGCCAGCCTCACCCCTCCATTCTCTCATGTCTCGCCAGCATCTCCTGTTTCTT - 5700
 5701 - TTGCGGGAGGTTCTCATCAGCCTGTCCCATGAGTCTCCATCTTCAAGATGCGCTGGCCT - 5760
 5761 - AACCGCCTACACTGCCAGCCGCTTCCCCCGTACCTCTATAAGAAGATGCGCTGGCCT - 5820
 5821 - GGAAGCCACCCAGAGGCCCTGGTGGGGACAAGATTCCCTTGTGGATTAGTAAGTCT - 5880
 5881 - CTTACCCAAATCAAAGTCTCCCTTTCTATGATGAATGCCAATATGACCTCCAAACCG - 5940
 5941 - TCACCAGCAAAGTGAAAGTGAGCCAGGGCCGAGGCAGTGGCTCACGCCTGTAATCCCA - 6000
 6001 - ACACCTTGGGAGGCCGAGGCAGGAGGATCACTTGAGCTCAAGAGTTTGAGATCAGCCTGG - 6060
 6061 - GCAAGATGGCAAGACCCTGTCTCAACAACAAAGAAATTCGCCAGGCGTGATGGCTGGCAC - 6120
 6121 - CTGTAGTCCCAGCTACTTGGGAGGCTTAGGCAGGAGGAGCACTTGAGCCAGGAATCAAG - 6180
 6181 - GCTACGGTGAGCTGTGATTGTGCCACTGCACTCCACCCTGAGTGAAGCAATAATCTGTC - 6240
 6241 - TCTTAAAAAAAAAAAAAGTGAACCAGGAACTAAAGGCTTTTGAAAGGCTACCTCTATT - 6300
 6301 - TTCTTAAAACCCACCTCCCACCAAAATAAAAGTTCTCATCTTAAAAGTAGGCTGGCAGG - 6360
 6361 - GAGAAAAGGCCTTGGAGTCACATTCCTACCTGAGAACTTCAGGGCAACTTCTGATGAGTT - 6420
 6421 - CCCACCTCAACTCCAAATTAAGCCCTCAACAGAAGTAGCTAGGAAGCTGATCACTTCT - 6480
 6481 - AATTACAGCTCCCTCCCTCCTAGCTACTTTCTGTGCTATCGAGATACTTGGGAAGACAC - 6540
 6541 - AGGCCAGAGTCCAGCCAATTCTGTGCCACAGATCCAGAAGCTGTGGTCCATCGGCCGATG - 6600
 6601 - GGTGCCCTTAGGACAGCCGAGGATGACCTTTATTCATGCTAGGAGCTAGGGCAATAGCA - 6660
 6661 - ACGTGGGCTGGGAGCTGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG - 6720
 6721 - AACACTTTGCTTCCCTTAGTAGTGATGACATTTTATTTGTGCCCTGAAAAGCACTTTCATG - 6780
 6781 - AGACCCAGTAACAACCCATGGAGATCTATGCTATTGGCCCCATTTAACAAGAAAAACAG - 6840
 6841 - GGTGCTCAGAGAAGTTGTACCTGCCAAGGACACACAGCTAGCAGAGCGAATGGACAGG - 6900
 6901 - TCAGGACCAGTTATTCAGCCTCTAGGAGCCATTACTAAGTCTCTGATCAACAAGGAAACA - 6960
 6961 - AGTTTCCCCCGGGGGTTTTTCCACCCGAGCTGAAACAAAGCCTCTTTCACCTGAGCCT - 7020

6961 - AGTTTCCCCCGGGGGTTTTTCCACCCGAGCTGAAACAAAGCCTCTTTCACCTGAGCCT

Fig. 23 (continued; 6/6)

7021 - CTCACTCAAAGGGAGGGACTCCCGAGGGGCAGGGGGCACTCAAGTCCAGGCCTGTCTATC - 7080
7081 - CCTGGCCCCCCCCACCCAGGATTTTGTGCCCGCACCGCTTGGGGACTACCAGCAGCTGCT - 7140
7141 - GACCATCGGCTTCGAGGAGCCACGCCCACGCTGGCCACCGACCTGCTGGTGCAGATCCT - 7200
7201 - CACGGGCCAGGCAGGCCAGGCCCGGCTCCGAGCGCAGCCGGGCCTGCGGGGTGGGCAGC - 7260
7261 - GCAGGGGTCTTGAACCTGGGGAAGAGGGGTAGGAGCTGGAACCTGACAGTTCCAACTCCA - 7320
7321 - GAATAGGGGGCAGGGGAGGGGCTCACTCGTTCTCGCAGTGCAGCCGGGCCTCGCCTTCCA - 7380
7381 - AAGGGCCAGGCCGAGCTGACCTGTCTGCACCGAGTCCGGCTTGGCCGTGGGGCCCTGAAT - 7440
7441 - GCGGACACGTCAAGTTTTGTGTTAAATAAAAGAAAGAAAGAGGTACAGGCTCAGCGTCCG - 7500
7501 - CTGCGAATGCCGCGCCCCCTCCCCGGGGGATTGCCCCACCCACTCGCGTGGCCTTCTGGG - 7560
7561 - AAATGTAGTCTTTTGAAAGAAGCCTGGAATTCGCCAATAGGCGGACGAGAGTTTGGCGCA - 7620
7621 - TGCGCATAGGCGCACATGAAGCAAAAAGGGAAGTGGTGCCCGTCAACACCGGAACCCAGA - 7680
7681 - AAAGTCAAGTTTAGGGTACCGGGGAAATTCAACGTCCACTGGAGGAAGAGACTTAAGGC - 7740
7741 - TACGCCCCACTCCCATATTTTGACCCGGAAGTTATTTATTTTAGCGTAGAAGACTACTTTT - 7800
7801 - CCCGACGCGCCCCAGGAAAGTGCCCTCGATCAGTTTCCTAAGGGCCCGAGTTAGACTTTT - 7860
7861 - TTTTCTCTTCCAGCTTTTGGGACTTGGGGGCCGGACAGGTCGTCTTTCTTGGGGTA - 7920
7921 - TCCGGGGTGCGGACAAGGTGGGAGAGCCCTACGGTATCCAAGCTT - 7965

CCGAGGCTGCTGCTATC

Fig. 24 (19)

1 - CAACATGCTTGGGACCAGAAGTGTTCCTCAATTTGGGATTTTCTCAAATTTTACCGGTTGA - 60
 61 - GCTTCCCCAATCTGAAAATCTGAAATCCAACATGCAAGGCTCTGAAGTCTTTCACTGAGC - 120
 121 - CTTTGGGGGAAATATTTAACATCCTAACAGCCCTAAACCAACGCTCAATTAGCACAACAG - 180
 181 - TTTACAATCTTCTCTACCCACAGCCTGATGCGAGSCTCTGGGACTAGACTATTTAGCCAA - 240
 241 - CAGTTCTTGCAAATTAAGTACTTATAAGTAAATAGTAATTTCAACACCTCACTGCTAA - 300
 301 - TGCTGTAACAACCTCTGCAGACCTAGGGAGCAAGTACGGTTTGAGAGCACTGGGAAGGCT - 360
 361 - CTGAAGTGACCTTTGAACTGGGCCTCAAAAAATTTGGGTTTGGCAAAGTCAAATCTCT - 420
 421 - TAGGCTTCAAATTCAGGCACAAGGATTGTTGGGTTGATTTCATTATCCAGAAGCAATG - 480
 481 - GGGATACAGAATTGTGATCTCATGTGTAGGGAACCTGCGGGGTTTTTCTACTTTAACCC - 540
 541 - CAGTGAGACTTTGTAGAGTGTGGGGTAGAGAAAAGCCTCATGAATATGCCTGAAGCCTAA - 600
 601 - CTCAGCACCTTTCTGAGGAACTGACTGCCAAAATGTAATGGAGAGGGGAAAATATGACC - 660
 661 - TACTTTTACAAGTTACCTTGACTGCCTCAGGGAAACCTGCTGTGGTAGTGTCTCTCTGG - 720
 721 - GTGAAAGACCAGGTAATTACCTGGGTGCTGGTCTCAGACTTACCAGTTTGAATCCCTGT - 780
 781 - TTTAACCCTCACTATCGATATGACCTTGGATAAGTTACCTAACCTTTCTCTTACTGTCC - 840
 841 - TTTTCCGTAAAATGGGGATAACAGATAGTAGTTATTTCTATGAGTGGTTATGAGAACCAA - 900
 901 - GCTATTAGATAGCGGGAAAGCACACAGTAAGCGTTCAAGGAACTGCTATTGTTATTAAAA - 960
 961 - GCCTCCTTTTGAAGAAGGACATTGAGGCCAGAGAGAGAAACAGAACGTCAGCCACACAG - 1020
 1021 - CAAATCCGTGATGAAGTTGGGACTGGAGTATGGGTCTCCTGAGTCTCAGCCCAGGACTCT - 1080
 1081 - ATCCCTCTTCCCGAGTCTCGGAGTTCCCGGATGGAGTCACATTTGTTTACGGCCAGGGA - 1140
 1141 - GGAAGGTTTGATGGAGGCTGCAGGAAACAACAGCCAGGCGCAAGGCTTTGGGAGTTGAA - 1200
 1201 - GCATAGCTTCTGCGAGATAGAAACAAGGTTGACATGGGCACTCGTGCAGAATGACGGGCT - 1260
 1261 - CCTTTTGGACTCCCAGGACTACAGTCCCTTATGCACCTTGGGATCTGCGGCTAGCCCTG - 1320
 1321 - CGTAAAGAGGGACGCGTAGTCTTTTCCCTGCCCGCCCTGCCGGGGCGCCCGCTCCGAG - 1380
 1381 - GCCGCCCTCGCTTCGTCCTTCCCAGCAAGCTCCGCGCCGGCGCCGGCTATTGATTGGCTG - 1440
 1441 - AGGCGGGAGCAGGCGGCTGGCCGGCAGCAGTTACTCGGGGTTTCGGGTGCGAGGCCAGAG - 1500
 1501 - GTGGGGAAGCCATCGGACGTCGGCGGTGAGGTACGTGCAGCGCGCGCGGTGGGCGAGAC - 1560
 1561 - TATTTGAGAGTGTGCGGGCCGGGATGTTCTCGGCCTGTGGGGAATCACGCCAACTCCCC - 1620
 1621 - GCGTGGGCGCGGGGCTGTCTGGGGATATGCGCATGCGCGGGCGTGCCTCGCGGCTTGAGG - 1680
 1681 - GCGCGCGGGGCGTGGGTGGCTGCGCGCGCGGGGGGCGCACGTGGGGCCTGAGGGGCGGGG - 1740
 1741 - GCGGTGCCGGGAGTCCCGCCACGTACGTCTCCGGCCCTGAGCCAATCCCGCGCCCGGCCT - 1800
 1801 - GCCGCGAGGGGGCCGGTTGTGCCGGGAAGTGGCTCCAGGGAGAAGAGGCCTCTTCCCTCA - 1860
 1861 - CCCGCTGTGGGAGCTGCGCCCCGAAAGCCTGCCCGGCGACGTGCGGCTCTCCTGACCCGC - 1920
 1921 - CAAGACCAGAGAGCCGTTGGCGCCCTCCGCGGGGCTGCCGGTCCGTTTATTTTAAAGAA - 1980
 1981 - GCTTTGTGCGCCTGCTGTGGGGATTTCTGATCCAGGCTGCGAAGAATTTCAAGTCTGGA - 2040

 2041 - AAATAGCAACTGTGTTTGTCTTAAAGGATCTTCTCCTGACCCAGCATCGCTCATCACA - 2100
 - M
 2101 - TGAAGAACCAAGACAAAAAGAACGGGCTGCCAAACAATCCAATCCAAAAAGCAGCCCAG - 2160
 - K N Q D K K N G A A K Q S N P K S S P G
 2161 - GACAACCGGAAGCAGGACCCGAGGGAGCCAGGAGCGGCCAGCCAGGCGGCTCCTGCAG - 2220
 - Q P E A G P E G A Q E R P S Q A A P A V
 2221 - TAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAGGGTGTGTGCCAGC - 2280
 - E A E G P G S S Q A P R K P E G
 2281 - TCTGCGTTGCCAGCGGGCAGGGGGAGGAGCTGTGGGGTGGCCCTCGCTTCTGGACTTACA - 2340
 2341 - GGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGTGGGGGCC - 2400
 2401 - GCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTTAAGCACAGGAACAGA - 2460
 2461 - GTTCTGGAGAGAAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGTC - 2520

Fig. 24 (continued; 2/9)

2521 - AGGAAATCCAGGTCCCGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCTGT - 2580
 2581 - TGAGGCATTTCTAGAATGATCTGAATGGCAAGAAATGGGTTTTGTGGGGGGAAGGAGAT - 2640
 2641 - GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATCT - 2700
 2701 - AACAAATATGTTCCGGTGGTAGTGAGAAATAGTTGTGTCAATTTTACAAGTAAACAGACTT - 2760
 2761 - AAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAGATGTTTCGAATCTAAAT - 2820
 2821 - TCTGACAGGAAGTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA - 2880
 2881 - AAAAAAGTTAGGCAACATTTAACTCAAACCTGATGAGTTTGGCTGGGCCTGAAAAATCCCA - 2940

2941 - ACCAGTGGTATAATCGTCTTCTTTCTCACTCTACCCCTCATCCTCTCCTGCTGTAGGGGC - 3000
 - A

3001 - TCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCA - 3060
 - Q A R T A Q S G A L R D V S E E L S R Q

3061 - ACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCGGCGAGGA - 3120
 - L E D I L S T Y C V D N N Q G G P G E D

3121 - TGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGTGGC - 3180
 - G A Q G E P A E P E D A E K S R T Y V A

3181 - AAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCAATGGAGAGAAGGAACCCTCCAAGGG - 3240
 - R N G E P E P T P V V N G E K E P S K G

3241 - GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCCGAGACCGAGACCATCGAAG - 3300
 - D P N T E E I R Q S D E V G D R D H R R

3301 - GCCACAGGAGAAGAAAAAGCCAAAGGGTTTGGGTGAGCAGAGGGCGGCTCTTTGTGAAGC - 3360
 - P Q E K K K A K G L G

3361 - TGGTGAGGAGAGGGAGTTTGGACTTGACGTTCTCTGGGCCAGTCTGTTCTGCCAGGATTC - 3420
 3421 - AAAGGAAAACGGTACTTCTCAGAGCAGCAAGTCACTCTAGTCTAATCAAAGCCAGGGATG - 3480
 3481 - TGGGGGCCACGGCATAGAGATGCAGGAGTTACCAGCACAAAGCCTTCTGGGTTTTGGA - 3540
 3541 - GCAACTGGAGCTTGGCATGGGACCTGTTCTCTCTTTGAGAAAATGGAGACGGGAGGCTAG - 3600
 3601 - GGTAGGCTCCTGTGCCAGCCAGTACTACCTGCTGTGTGACCTTGGGTGTGTCCCTTCTCC - 3660
 3661 - TCTCTGGGTCTTAGTTTATATTTCTCTTTACAGTAAGAAAATTAGACTAGGCCAGAGTTG - 3720
 3721 - AAAACCCAAATATCTGCATAAGCTGGGCTTGGCCATGGGGCCACCTGAAGATGGAGGCTT - 3780
 3781 - TACTGCTTCCCTGATTAGTTGCTCTCACTAGCCAAGTACAGGAGCAGGCAAACTACAGGCT - 3840
 3841 - GGGTGCAGTCAGGCTTTTTTTTTTTTTTTTTTTTTTAAATAAAGAAAAGCCAGAAATCT - 3900
 3901 - AGAGTTATGTGAGAACTCTAGATTTTTTCATAGTTAGCAGCTAAAATGGTAAGAGCCAAA - 3960
 3961 - CAAAACCCATCCGTGGGTGGATTGTCACACATGCCTGCCAATTGCAGTCTCCATGCTG - 4020
 4021 - ATCTCTTGGGCCCTTCTGGGAGGCAGAGGGAAGGCTCCCTGACTCAGTCACAGGCAATG - 4080
 4081 - GGGAAATAGGCAGTGACAGTCATTTTACAGCAGGGTATGTATGTTTAAGAGTCTAGGCCGG - 4140
 4141 - GGTGTGGTGGCTCACGCCTGTAATTGCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACC - 4200
 4201 - TGAGGGTCAGGAGTTCGAGAACAGCCTGGCCAACATGATGAAATCCCGTCTCTACTAAA - 4260
 4261 - ATACAAAAATTAGCTGGACATGCTGGCACACGCCTGTAATCCCAGCTACTTGGGAGGCTG - 4320
 4321 - AGGCAGGAGAATGGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGTGAAGATTGTGCCAC - 4380
 4381 - TACATCCAGCCTGGGTGACAAGAGTGAACTCTGTCTCAAAAAAAAAAAAAAAAAAGAATCTA - 4440
 4441 - GAATCTAAGTCGAGTGTCAATATATCCATGTTTTATTTCCTATTCCCTTTTCCCTTATGT - 4500
 4501 - ATCCTCTTACTTTAAAGAGGAACCTTAAAGAAATCTTAGGGACGACTAGGCAGAGTGGCTC - 4560
 4561 - ACACCTGTAACCTCAGCACTTTGGGAGGCAAGGCAGGAGATTATGAGGTGAGGATTC - 4620
 4621 - GAGACCAGCCTGGCCAACATGGTGAAACCCAGTTCTACTAAAGATACAAAAATCAGCC - 4680
 4681 - GGGCGTGGTGGCACGTGCCTATAATCCCAGATACTCGGGAGGCTGAGGCAGGAGAATCAC - 4740
 4741 - TTGAACCCGTGAGGCAAAGTTTTTCAGTGAGCTGAGATCATGCCATTGCACTCCACCTGGG - 4800

Fig. 24 (continued; 3/9)

4801 - TGACAGGGTGAGACTCCATCTCAAAAAAGAAAAAGGAAAAATCTTAACGTCACATACA - 4860
4861 - TGGAAAGATCATCTTTTTACCCCCCACCCTCACTGAGATGGAGTTTTGCTCTTGTCAC - 4920
4921 - CCAAGCTGGAGTGCAGTGGCGCGATCTAGCTCCCTGCAAGCTCCGCCTCCCGGGTTCACA - 4980
4981 - CCATTCTCCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTGCTACCATGCCC - 5040
5041 - GGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCATCTGTGTTAGCCAGGATG - 5100
5101 - GTTTTGATCTCCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTGTGGGATTACA - 5160
5161 - GCGTAAGCCACTGCACCCCGCCTTTTTTTTTTAATTAATTAATTTTTTTAGACAGAGTC - 5220
5221 - TCGCTCTGTCCCAAGCTGGAGTGCAGTGGCGCGATCTGGGCTCACTGCAACCTCCGCCTC - 5280
5281 - CTGGGTTACGGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTG - 5340
5341 - CTACCATGCCCCGGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCACTGTGTT - 5400
5401 - AGCCAGGATGGTTTTGTATCTCCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTCC - 5460
5461 - GCCTCAGCCTCCCAAAGTGTGGGATTACAGGCGTAAGCCACTGTACCCTGCCTTTTTTTT - 5520
5521 - TTTAATTAATTAATTTTTTTAGACAGAGTCTCGCTCTGTCAACCAAGCTGGAGTGCAGTGG - 5580
5581 - CGCGATTTGGGCTCACTGCAACCTCCGCTTCTTGGGTTCAAGCGATTTTCTACCTCAGC - 5640
5641 - CTCCGGAGTAAGTGGGACTACAGGCGCGTGCCACCACACCAAGCTAATTTTTTTGTGTAT - 5700
5701 - GTCTTTAGTAGAGATGGGGTTTACCATGTTAGGATGGTCTCGATCTCTTGACCTCGTGA - 5760
5761 - TCCGCCTGCCTCGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCTTGCCTGGCC - 5820
5821 - GAAAGTATCTTCATTTTAAAGTTCAGTGTTTGGCTACTCTGTTGACAAGAGTTTAGTATT - 5880
5881 - TCTCAAGGAGGCTAAGATACCTATTCTTTTGGATCCTACCTCTATCAGGAGGGTGGGC - 5940
5941 - CTTCTTGCATTGAAACAGTATGAAACAGTAGCCCTGAATTCATAAGTGGGACACCTTT - 6000
6001 - CTTCTATTGGTAGAGCAGGCAGTTTTTTTCTCCTGCCAATGGTGCCTACTAAGGAGATTT - 6060
6061 - CACTAGGGTACAGTCGTTTCAATTTGATAAGCATTTGTTGAGCATATCCTCTGTGATGGTAC - 6120
6121 - TATGGACAGTACTGGGGCTATAGTGAGGGCAGGATTGAGTTGGTCTTATGGCAAGGAAG - 6180
6181 - GCAGCTAATCAACAAGCAAAATATAAAGTATGATGGGGAGGGCTGTCTTCAGCACTCATG - 6240
6241 - AGTGTGAGCCCAGGCCTGGAGGGGACACCTGGAGAAGAGGGTGCATGTCTTTGCTCCTGT - 6300

6301 - GCTTTTCAGGGAAGGAGATCACGTTGCTGATGCAGACATTGAATACTCTGAGTACCCCCAG - 6360
- K E I T L L M Q T L N T L S T P E

6361 - AGGAGAAGCTGGCTGCTCTGTGCAAGAAGTATGCTGAACTGGTCAGTTCCCCCTCCGCG - 6420
- E K L A A L C K K Y A E L

6421 - GGCACCTTCCCTGCGTTGGGAAAATCAGCATGCCACCTGGTGTAAAGTTGGGGGTGCAGA - 6480
6481 - GTCAAGTAGGTGGCTTAATTCTGTTTCACTTTTCTCTGAACATCTGTTAAATGGGGAA - 6540
6541 - TCACTTCCAGGACCTCTTTCAGGGCTGTGCAGCAAGAGGAGAACTGCATATTCTTGA - 6600
6601 - AAGAAATTTCTCAAAGATGATTCCAAGGTGGTAGAGCCCTTGTTCCTGGCCTGAGTCCA - 6660
6661 - AGACACCTTGTGATCTTGATGCTTCTTCTCAAATACAGATGCATAGAGCCATTATCACA - 6720
6721 - GTTAATAAACTAACACTAGTCACTTGATACTTTTTCTTTTACTCCAGAGCAGTCTTCT - 6780
6781 - TGTCAGTGCCTCCTCATATTCCCCATGACATTGACTTTTAACAGAACTAGACTAGCTGT - 6840
6841 - CTTGTAGGATGCCCCCTTCTAGCTTTGTCTCTCTGTGGTATCATTTTACTTCTTTACCT - 6900
6901 - CCTGGTACATGTAAGTGAAGTAGAAGTTAGCTCTAAAGCTTGATCCAATTCAGCTTCAAC - 6960
6961 - TTTTTGACAAGAATTCTTCATAAGTACTTCATGTTCCATCACAATAAATGCAAAGCATGC - 7020
7021 - TCTTCCCACTTTGTTGTAACATTGTTTCACTGGGTTGGGGGTGGGGCAGCCAGATTCTTCC - 7080
7081 - ATCATCAGGTCCCTTGTGAGAATTTGAACAAACAGATTTATCCATTGATGGTCACAGCCT - 7140
7141 - GTGTATGTATGTATGTATGTATGTATGTATGTATTTATTTATTTATTTATTTTTGAGAC - 7200
7201 - GGGGTCTTGCTCTGTGCGCCAGGCTGGGGTGCAGTGGCACGATCTCGGCTCGCTGCAAGC - 7260
7261 - TCCGCCTTCTGGGTTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGTCTACAG - 7320
7321 - GCGCCCGCCACCATGCTAGGCTATTTTTTTTTTTTTTTTTTTTTTTTAGTAGAGACGGGT - 7380
7381 - TTCACCGTGTAGCCAGGATGGTCTCGATCTCTTGACCTCGTGATCCGCCCGCCTCGGCC - 7440
7441 - TCCCAAAGTGTGGGATTACAGGCTTGAGCCACCACGCCTGGCCTATTTATTTATTTATT - 7500
7501 - CAGAGTCAGAGTCTCGCTCTGTCAACAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCATT - 7560
7561 - GCAACCTCCACCTCCAGGTTCAAGCGAGTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA - 7620
7621 - TTACAGGTGCATGTACCATGCCTGGCTAAATTTTGTATGTTTTAGTAGAGACAGAGTTT - 7680

Fig. 24 (continued; 4/9)

7681 - CAGTATGTTGGCCAGGATGGTCTTGATCTCTTGGCCTCGTGATCCGCCCCGTCTCAGCCTC - 7740
 7741 - CCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGCCTGGCCTCTAAGTATTTATTTTAA - 7800
 7801 - AATTAATTCATTCCACACACATTTATTAATATTTTCCTGTAAGGAACCTTACTCATCTTT - 7860
 7861 - AAAATGGGGAATGTCATACCTGCCTAATGACATTCTTGTAAGGATTAAATAAAAAGGTATA - 7920
 7921 - AGGAAGATAAGCACCCCTTTTGGAGTGATCCAGCCAGGGGAAAATTGCTGATGCAAGAGAG - 7980
 7981 - GAAATGAGTTGCTAGAGTGGTGTGTGTAGTAGAGGAGGGGAGCTGAGGCCTGCCCAAGAA - 8040
 8041 - GGGGGCTTGGCTGTGGTAACCACATGGCTAGGTCTGTGTGACTGGAGGAGAGGACGGGGC - 8100
 8101 - AGGTGGACTGGTAGATGTGCAGCTTGTGCCCTGATTCTCTAGTTTCTTCTGTGTTTTGA - 8160
 8161 - GATTTGATGAGAACGATGAAATAGTTGTCTGGAAGGAGAGGAGTGTGAATAGCATATGCA - 8220
 8221 - TTGTATTGGGATTGCTGGTCTTCTGAAATTGGTGGCCATGAATTTAAAGTGAGACTCTT - 8280
 8281 - CAAGTAGGGTTGTTATAGTACTGGTGTAAAGCAGGAAGGTGCTTTACTAGGGTTGCAGTA - 8340
 8341 - CTACTGGGGAAGGGCCAAGAGAGTTGAGGGTGTAAAGAAATCCAAGCCAGGTAATGTAGTT - 8400
 8401 - ATTTTAAAGGAGAGTGGAAGGATGGTTGAGTCAATGGATTGGAGGTCTATAGGGTAAGA - 8460
 8461 - GACTTTCTGAGGATCACAGATACTGATTGGAATGAGCTAAAAAGATAGGTGATGGTAGTC - 8520
 8521 - CTGGACTGGGATGCTGGAAATTGAGATAGTGGGTGTGCTCTCTGGTAGTGACAAATCTAG - 8580
 8581 - ATCTGCGCTGTCCAAGATAAATTCGTCTCTAGCTAATTGACATGTGGCCAGTTTGAATTT - 8640
 8641 - GAACATGCTATAAATGTAAGATACACATCAGCTTTTGAAGACTTAAGCAAAAACAAAGAA - 8700
 8701 - TATAAAACATCTTTTTGTGAGAGAGTGTCTCAGTCACCCAGGCTGGAGTGCAGTGGCGTG - 8760
 8761 - ATGTCCTGCTTCCAGGTTCAAACGATTCTCCTGCCTCACAGCCTCCTGGAGTAACTGAGA - 8820
 8821 - TTACAGGCGCATGCCACCAAACCTGGCTACTTTTTTGTATTTTTTTTTTAGTAGAAACGGT - 8880
 8881 - TTCACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTCAAGTGATCTGCCTGCCTCAG - 8940
 8941 - CCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACTCCCGGCCTCACTTTTTTACAT - 9000
 9001 - TGATTCCGTGTTGAAATTGTAATGTTTTGGATATTAGGTAAATACATATATTACTAAAA - 9060
 9061 - TTAATTTACCTGTTTTTTACTTTTTTAGTGCGGCCAGTAGAATATTTTAAATTACTTAT - 9120
 9121 - GTGGTTTGCATTATATTTCTGTTGTACAGGCCTGGATAGGGTCATGGGAGGGGAAGT - 9180
 9181 - CTGGGAAAGGAGTGGGTTTGTGGAAGAGGTGATGGACTGTGAGGCCAGGGAGTTAGAAG - 9240
 9241 - GATTATCTGTTGATACTGAAGTGGCCACAAATGAGAAAAGTAATTGTGTTGGGGAGAGCG - 9300
 9301 - CTGATGAACGCAGCGCTAACGTTTTGAAGGAATGCGAGGGAGCGATGGGGGTCTGTCTGT - 9360
 9361 - TAATAGGCACAAGGTACGGTAGCAGGTGGTCTCATCCTCGGGCATGAGTGTCCAGCAAGT - 9420
 9421 - TGGGGAAATGCAACAGCTTGAAGTGGCTCTAGTGGCCCAGAGTCAGAGCTGGAATAGGAA - 9480
 9481 - TTGGCATCTGCTGGCTGTGTGGCCCCCTGCTTGCCTAGTGAGTTACCATTTCTGTCCC - 9540
 9541 - TACGGTGGAGCCTTTGGGGTTATTGTGAGTTCATGGGAGGAGCGTGAAGCACCGGCACA - 9600
 9601 - GCATCAGCCCATGAGAGTGCTCCTGGCCTGAGAGGGTAAGGGTCAGGCAGCTCAGGAGA - 9660
 9661 - CCCTAGACCTGCATAGTGATCCCCCACCAGGAAGGCCCCACAAGATGCTCACCTGCCCT - 9720

 9721 - CCCTATCCCTGTCCCCAGCTGGAGGAGCACCAGGAATTCACAGAAGCAGATGAAGCTCCTA - 9780
 - L E E H R N S Q K Q M K L L
 9781 - CAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCACCTGCGCGGTGAGCACAGCAAG - 9840
 - Q K K Q S Q L V Q E K D H L R G E H S K
 9841 - GCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGC - 9900
 - A V L A R S K L E S L C R E L Q R H N R
 9901 - TCCCTCAAGGTAGGCCTGGGCCCCCTGGAACAGGTGACTCTGGTTTCCTTGACTTCCACT - 9960
 - S L K

 9961 - TAATGTTTCTTTTCATGGGCTTTCTCTTAAAAAGTAGTGCAGGCTAGGGCCAGGCGCAGT - 10020
 10021 - GGCACACATAAGTGATTAAAAATCTTCTGGCCACTAAAAAACAGAAATTAATTTTAGTAA - 10080
 10081 - TATACTTAACCAATATCCAAACATTACAATTTCAACATGAAATCAGTGTAAGGAGCA - 10140
 10141 - AGGCTGGGTGTGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGATGG - 10200
 10201 - ATCACTTGAGGCCAGGAGTTTGGAGACCAACCTGGTCAACGCAGTGAAACCCCATTTACT - 10260
 10261 - AAAAATACAAAAATTAGCCGAGTGTGCTGGCAAATGCCTATAATCCAGCTACTCAGGTG - 10320

Fig. 24 (continued; 5/9)

10321 - GCTCAGGCATGAGAATTGCTTGCACCTGGGAGGCTGAGGTTGCAGTGAGCCGAGATTGCA - 10380
 10381 - TCACTGCATTACAGCCTGGGCAACAGAGTGAGACTCAGTGTCCAAAAAAAAAAAAAGTA - 10440
 10441 - GTGCAGGCTTGTGGCATAGAAATACACTTTCTCAATAATGCCTTACGTTAAGAGAGTACT - 10500
 10501 - GCTTGTAAATCATTTTGACATGTATTAGATAAGGTGAAGGATAAAGTACTAAGAGAATCCAT - 10560
 10561 - AATGCACTGGCGTTAGTATTTCTCAATGAAATGACAGTCCCCTGGTAAGCGGAGGCCTGG - 10620
 10621 - CTCTGACAAGCAGCTCTTGTCCCAGACGTTGGTCAGTCAGGAACCTGGGTCCCTTCCCATG - 10680
 10681 - TTCTGCTGCTTCTATGGTGAGGTGAGTCTGTGGTTACACCAAGTTTAAATACAGCCTTTT - 10740
 10741 - AACTTTCTTTTTTATATGTAAATCTTACATGTAGTTTTTGAATGAAATTATTATACAT - 10800
 10801 - GTACCATTTTCATATCCTGTGCCTTTTTTTTCACTTTACATAACATTTTTCCCTATCAGTAT - 10860
 10861 - GTGTAGGGCTATCTTCTCATTATATGGATATATTATATCAGTGCCCTAGTTAAAGCATT - 10920
 10921 - TGGGGGTTGTTTACAATTTTTTCAATTATACATATAGAACTATAGTGAATTTCTTGTAT - 10980
 10981 - ATTTATCACTGGTCAGTTATATAGAACTTATCTGTAGGATAAGTCATGGAATTGAAATGG - 11040
 11041 - CTAGGTCACAGTATATGCAGATTTTTTCATTTTAATAGATTTTGCTGGATTGCCCTCCAGT - 11100
 11101 - GAGGGGGCAGTGTGCCTTCCCCATCAAAGTGTTGAGTGCCTAATTCTGCACAACTTTGC - 11160
 11161 - AAACCTGGGTACTAAATTTTAAACAGCTTGGTCTCTGGGGGTACAGAGGGGACAAAT - 11220
 11221 - GCACATTAATCTGAAATCTGGAAGAATAGGCCTTAGGAGATCCGACTTGCTTCAGAATGG - 11280
 11281 - CACTTAGCACTTACATGTGTGCATGTGTGCCTGCATTTTTTCTTCTTTTTTTTTTTTG - 11340
 11341 - GGGACGGAGTCTTGCTCTGTGGCCCATCGCCCAGGCTGGAGTGCAGTGGCGCGATCATAG - 11400
 11401 - CTCACCACAACCTCCGCCTCCCAGGTTCAAATGACTCCTCTGCCTCAGCCTCCCAAGCAG - 11460
 11461 - CTGGGACCACAGGTGCACACCATCACGCCGGCTAATTTTTGTATTTTAGTAGAAACGGGG - 11520
 11521 - TTTCACCATATTGGCCAGGCTGGTCTCAAACCTCTGACCTCGTGATCCGCCACCTCAGC - 11580
 11581 - CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCTGCCATGTGCCTGCATTTTT - 11640
 11641 - CTAGGGGGAGAATCTCACTTGATGTACCTGATATACAGAGGGGGCCATTGGAACCCGCA - 11700
 11701 - TTGCACAACATCCTGGAGTCTGGCTACTCCACGCTTTGGGAGCAGGAGGGCTGTTGGCA - 11760
 11761 - GAGACCATCTGTGGACTAGCTGGGGGACCCTTGTGAGGTAGCAGTGGATGATGGCTCTCG - 11820

 11821 - GGCTGACTTCTTTGCCAGGAAGAAGGTGTGCAGCGGGCCCGGGAGGAGGAGGAGAAGCG - 11880
 - E E G V Q R A R E E E E K R
 11881 - CAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACA - 11940
 - K E V T S H F Q V T L N D I Q L Q M E Q
 11941 - GCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCTGAGAGGCTCAA - 12000
 - H N E R N S K L R Q E N M E L A E R L K
 12001 - GAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGGTAAGGGTATCACGGACAGCAGTCAT - 12060
 - K L I E Q Y E L R E E

 12061 - GGCCCAGAAATTGTGAGGTTTTGAGTGTGTGCTAGGCACTGGGACAGTACCTTTTCAGGC - 12120
 12121 - TTCATCCCATTCTCCCTTTCTTCTCCTCCTCCTCCTTGGGAGGAGAGTAATGTTATTCC - 12180
 12181 - TCATAGATAAAAAACAGGTGTGGAGAAGAGACTCACTTACAGCCACACAGCCCCAGGTCC - 12240
 12241 - ACAGTGCCCTTGTCCCAAATGACTGGGCCAGGCATCTTTTGAATTAGAACTATCCACATT - 12300
 12301 - TTAGAATGGAGGTACATGTATGGAAGTGTGTATATAGCACCCTCAGCAGGGCCTTGGG - 12360
 12361 - GAAGCCAGACACATTAATGTATTTATGCAGTAGAACTTCCAAATACTCACCTACATTATG - 12420
 12421 - GGCTTACAATGATGCAGGTCAAGTCTGGCTGCCAGCTTATGACAATTTCCATTTTCAGAA - 12480
 12481 - CTTTGTAGAATTTGGAATTGCAGGGGAGGGGTGTACCTGTGATCAGTGATGGACTCCAGA - 12540
 12541 - GACTGTGTCCACTGATTCTTGTCTGCTCCTGCCACTCAAAGGCAGAATTTATCAGGCTG - 12600
 12601 - GGCGTGGTGGCTCATGCCTGTGAATCCCAACACTTTGGGAGGGCCAAAGCGGGCGGATCACC - 12660
 12661 - TGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAA - 12720
 12721 - TACAAAAAATTAGCCAGGTGTGGTGGTGCACGGCTGTAGTCCCAGCTACTCAGGAGGCTG - 12780
 12781 - AGGCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAATGAGCCAAGATTGTGCTAC - 12840
 12841 - TGCACTCTAGCCTGGGTGATATACCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGC - 12900
 12901 - AGGATGTCACTCCCTTTGTCACTGCGTTGGCTGCCACCCAGGCACTTGAATCTTTGGAT - 12960

Fig. 24 (continued; 6/9)

12961 - CTTCCCTGCCAGTCACCTGGCTGTTCTGGGCGCGTTCTCATCATGAGAAGGGAGACCTGC - 13020
13021 - AGCCCCCTTACAGGGCTGGCAGAGGACCTGCTCTGGATTAGGCCCTTTCCTAGCCCCCTGG - 13080
13081 - GGTGTGGCAGTGGGTGAGACCGGGAAGATCTGCCCTCTTAGGTTTCATAGGCCAAAGTGAT - 13140
13141 - GATCGTGTGTGCAGGACCTAGAGGGCGCTCCCCTGACCCACCCCTTTCCCTGCCATACTT - 13200
13201 - CATCCTCTGGGAACAAAGCTGCTTGTTTGGTTTGGGGGAGTTGGTTTGGTTCTTATCCC - 13260
13261 - TCAGCGCTGAGACATAGAGGCTTCTGGGCCACTACAGTGAGACACGAACTTCAAGAATC - 13320
13321 - TGAATACCCCCGTTTTCTCTCCCCGCCAAGGCAAAAAAGGACTTAGTACTACCTGTGGAG - 13380
13381 - AAGGAGGTGCAGGACTACCAGGCCCTGCTGCTTTGCATTTACAGCCCTCCCCAGACAGAC - 13440
13441 - ACAGGCACCTCATCATACCCAACTGGACTTACCTGCTAGGCACCTTCCCTTCCCCATC - 13500
13501 - CAAAAAATGGAGTTATTTTCCCTTATTTTACAGCAAGTCCAGTTGATTTTACCTTTGAAGT - 13560
13561 - AGCACCTGAGTCCTTACCTTCTCTCCATCCCTTCTCTCTCACCTGACACAGGTCTGCAG - 13620
13621 - CGCTCCTCTAGTAGGCAGGACAGCCATTCTTGGGGATGCACATGTCTAGTCTTTGCCTA - 13680
13681 - GATATGGCAAGTCTTTGCCAACTGAGCTAGGCTGTTATGTTCTTAGAGGCATTGTTTTTG - 13740
13741 - CCCATTCTTCCCATTTACAAGAGAATCAGGGACACAGAAGTGAGGGCTTCCAGCCCCATA - 13800
13801 - GGTGATCAATCCTGGGGTCAGAGATTTGAGTGTGTTTATTGCTTGCCCTTCTGGGAGCAG - 13860
13861 - ATTCCATCCATAAACCATGTGCTTACCAAGGTCTGACTCACTGGGAGAGAAACGACGTGA - 13920
13921 - GGTGGAAAGCTGACCTTCCAGAGACTTGGGGCCCATGTTGTGTGGTACACATGGGAGTC - 13980
13981 - CATCATATCAGATTGAGATGGGGGGCTGGGCAAAGTGCCCTGGTCTGTGGCTGTGGGGCT - 14040

14041 - ACCCTGAGAAAGGGAGCGCTGACAAGCCGACTGCTCCCACCATCTTTGTTGCAGCATAT - 14100
- H I

14101 - CGACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGTCCAGCA - 14160
- D K V F K H K D L Q Q Q L V D A K L Q Q

14161 - GGCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTTGTGAG - 14220
- A Q E M L K E A E E R H Q R E K D F

14221 - GCTCAGGCCCCAGGGTTGGGGTGGGGGTGTGGGAGGAGACAGGCTGGGCTCTGGCTCAGC - 14280
14281 - TCATAGCCGGGTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTTGAGTACCA - 14340
14341 - GTCTGAGAGCAGGAAGCCTCAGTGGGTCTGGTGTCTGTGGCTAAAAACCAACATAGCCC - 14400

14401 - CTGGGGGCTTCTGACAGGATCTGGGGTCTGTCTTGGAAATAGCTCCTGAAAGAGGCAGT - 14460
- L L K E A V

14461 - AGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCACCTGAAGCAACAGGT - 14520
- E S Q R M C E L M K Q Q E T H L K Q Q

14521 - GAGAGCATATAACCTGACCCTGTGCCTTCAAGTTTCCCTCACTGGGCCCCATCCTGGGGG - 14580
14581 - TAGTGAAATGGGACCTCATTCTAGGACTGGCTGTGTCTGGCTGCTATGACGCCTTGGT - 14640
14641 - TGAGCTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCTTTTGAGGA - 14700
14701 - GGTAGGAACAGAAGAGTTTGAAAATCAACATAAAGGCAAAATAAAAGTCACCCTAAGTCT - 14760
14761 - CCTACTTCCAGGCTTAGCATTTTGGATTATATCCTTCCAAATATATAGCTTTGCTTTGT - 14820
14821 - TTTAAGGAAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACGGGTCTGAG - 14880
14881 - TGTGTTGACCAGAGTGCCCTCCCAGAGAAACCCAGTCTTATCTGTGGGCTGCTTTCTCCCC - 14940

14941 - ACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCAGAACACACTTTCCAAAAGCAG - 15000
- L A L Y T E K F E E F Q N T L S K S S

Fig. 24 (continued; 7/9)

15001 - CGAGGTATTCACCCACATTCAAGCAGGAGATGGAAAAGGTAAGTGTGGTCCAGGCCAGGCA - 15060
 - E V F T T F K Q E M E K

15061 - TGGCTGCTGGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCTTCAGGAAGCTCC - 15120
 15121 - CATCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTACAGCCTTTCCCCCTCTTGAG - 15180
 15181 - GCAGTATCAGTGGTATGTATACACTCCAGGTTGTCCCAGGGAATGGGGCAGTCTTTTCTG - 15240
 15241 - TTTGTTTGGTTTTTTTTGGGGGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGA - 15300
 15301 - TGGAGACTCACCTATTGCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTCATTGCAGCC - 15360
 15361 - TTTGCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGACTAGCTGGAATTACAG - 15420
 15421 - GCGCGTGCCACCATGCCTGGCTAATTTTTTCTTTCTTTTTTTTTTGTATTTTGTAGTAGAG - 15480
 15481 - ACGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGTGATCTGCCC - 15540
 15541 - GCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCATGCCTGGCCCCCTTACC - 15600
 15601 - ATTCTTGTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGAGGTGGCACAGAGGGC - 15660
 15661 - ATTGACTGCATCCTGTAATGCCTTGCGCCTTGGGATCAATCATTCACCTTGGAGACA - 15720
 15721 - CAGGTGCAGTCCCCACCTTGGAGACACAGACCTTGGAGAGGCCAGCTCTGACCATTTCCT - 15780

15781 - TCTGTCTGTACATAACCTAGATGACTAAGAAGATCAAGAAGCTGGAGAAAGAAACCACC - 15840
 - M T K K I K K L E K E T T

15841 - ATGTACCGGTCCCGGTGGGAGAGCAGCAACAAGGCCCTGCTTGAGATGGCTGAGGAGGTGG - 15901
 - M Y R S R W E S S N K A L L E M A E E

15902 - GCTGTCTGTGATCTGCAGCCAGGGTGGGGGTGTGCACTTAGCGCATATCAGGCCCTTTCC - 15961
 15962 - TGTATGTTCTACCCATCAGTGACACAGCTAGCATGAGGTAGAGGTGAGATTTGCACACAA - 16021
 16022 - TGTCCAAGTCCAAAGTTAATGCTGTTCTCTCCCCATGGGAGGTGGTGAAGCCAGTGGTAG - 16081
 16082 - GTCTCCAGTGGGAGTGAAGGGAGCAAATGGAAGAAAGGAATAAAAGAGCAGAAAAAACG - 16141
 16142 - GGTGCCAGTGATGTGCCTGGTTTACATGTAAAGCAGCCAGGTAGTTTGTGATTTACAG - 16201
 16202 - CTTGTAATGTAGAAGAAAGGAACATAACGATGGAGCAGCAACTGCAAGCCAGACCTTGCTG - 16261
 16262 - AAAGTTTTTGGGTTTTTTTTTGTCTTTTTTGTCTGCTGAATGTTTTTAGGTACGTTGTTTCAT - 16321
 16322 - TGAACCTTCTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAGATGAGACAGG - 16381
 16382 - CTCAAAAGTCAAGTCCTTTGCCAAGGTACGTGGTAGATAAATGGAGGAATACGTTATCT - 16441
 16442 - CCAAGCCGTGCCCCCTTTCTGCACCATGCTGCCCCACCTGACAGCCTAGTCATGGCTTCA - 16501
 16502 - ACTAGGACTGTTTCTAAAGGGGGCCAGCTTTGGACTCGGTCTGCTCTCAGCCTTGTTAA - 16561
 16562 - AGTGTTCGCCCAAGTGGTGATGGTAAGTGGGAGGTTGATGGGGCACGGCACTGAAGGT - 16621

16622 - CTCATTTCTTTCCCTAGAAAACAGTCCGGGATAAAGAACTGGAGGGCCTGCAGGTAAAAA - 16681
 - K T V R D K E L E G L Q V K I

16682 - TCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGACAGAGCGCAATGACCTGAACAAGA - 16741
 - Q R L E K L C R A L Q T E R N D L N K R

16742 - GGGTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTCACTGACAGTGGCCCTGAGAGGA - 16801
 - V Q D L S A G G Q G S L T D S G P E R R

16802 - GGCCAGAGGGGCCTGGGGCTCAAGCACCCAGCTCCCCAGGGTCACAGAAGCGCCTTGCT - 16861
 - P E G P G A Q A P S S P R V T E A P C Y

16862 - ACCCAGGAGCACCGAGCACAGAAGCATCAGGCCAGACTGGGCCTCAAGAGCCCACCTCCG - 16921
 - P G A P S T E A S G Q T G P Q E P T S A

16922 - CCAGGGCCTAGAGAGCCTGGTGTGGGTGCTGCTGGGAAGGGAGCGGCAGCCAGCCAGG - 16981
 - R A *

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Fig. 24 (continued; 8/9)

16982 - CCTGGCCCATAAAAGGCTCCCATGCTGAGCAGCCCATTTGCTGAAGCCAGGATGTTCTGAC - 17041
 17042 - CTGGCTGGCATCTGGCACTTGCAATTTTGGATTTTGTGGGTCAAGTTTACGTACATAGGG - 17101
 17102 - CATTTTGAAGGCCTTGCAATGCATTTATACCTGTAAGTGTACAGTGGGCTTGCAATTGG - 17161
 17162 - GGATGGGGGTGTGTACAGATGAAGTCAGTGGCTTGTCTGTGAGCTGAAGAGTCTTGAGAG - 17221
 17222 - GGGCTGTCTATCTGTAGCTGCCATCACAGTGAGTTGGCAGAAGTGAAGTCTTGAGCATTCTCT - 17281
 17282 - GTCTGATTTGAGGCTCAGACCCCTCCCTGCCCTTCAGAGCTCAAGACAAGTAATACACCC - 17341
 17342 - AGGTCTTGACTGCATTTGTCTTGTGAGCAGGGCTTGCTTGGTCAGCTCAGGCCCTCCTAG - 17401
 17402 - CTGCTCTGGAGGCTCCTTTGATTCTCTAGACCTGGAAAAGGTGTCCCTAGGCAGAGCCCT - 17461
 17462 - GGCAGGGCGCTCAGAGCTGGGGATTTGCTGCCTGGAAACAAGGGACCTGGAGAATGTTTTT - 17521
 17522 - GCGTGGGATGATGTGCTGGTCAGGAGCCCCCTTGGGCATCGCTTCCCCTGCCCTTTGGTAG - 17581
 17582 - TGCCAGGACCAGGCCAATGATGCTTCTCAGTAGCCTTATCATTACAGGTGCCTCTCTAG - 17641
 17642 - CCTGCACAAATGATTGACAAGAGATCACCCAAAGGATTATTTCTGAAGGTGTTTTTTTCT - 17701
 17702 - TTATTTCTTTTTCTTTTTTTTTTTTTTTTTTTTTCTTTTTCTTTTTTTTTTGCACATGACAGTGTT - 17761
 17762 - TGTATTGAGGACCTTCCAAGGAAGAGGGATGCTGTAGCAGTGGTGCCTGGGTGCCTGGCC - 17821
 17822 - TCCAGTGTCCACCTCCTTACCACCCCACTTGGCTCCTTTGCCATCTTGATGCTGAGGT - 17881
 17882 - TTCCTGTTTGGTGAGATCAGGTGTTTGTGGTAAAAGAAAGGAAAGGGCTTCTGATGGCT - 17941
 17942 - TTGCCACAAGCTTACCTGTGGGTTCAGCTCCTGAGAGGCCACCACAGTTCCTCATCAGCA - 18001
 18002 - CTGTCTCCATGCAGCAGTTGCTGGGTCCCCTGAGAGCTGCCTCTTTGGCTTATGGGTT - 18061
 18062 - TTTCTGCTTCCCTGCCCCCACCACCATGTGCAATCCTCAAGATTTGTCCTGATTCATT - 18121
 18122 - TCCTGGCACCTCCCTGCCTGTCTTGGGGATTCTACTTCTTCTGCTGTGGGAGCCCCATAG - 18181
 18182 - CTGTTGTCTAACAGGTAAGAAATGAAATTGAACTATTGACTGGGCCCCAGAAATCCATAA - 18241
 18242 - AATGGCTGCAGACAGTTGTTTCTGTGTCTGTTCTACCCCCACTCCAGTACATAACTACT - 18301
 18302 - ATGTACTGTGTAGAGCCATTCTATATGCTGAATGTTCTGCTGTTGCAAACTTGCCAGGGT - 18361
 18362 - ATTAGCCAGTGTGTTGTTGCCAAGCAGTTTTCTGGGACAACAGAATGACTCAGACCAAGATG - 18421
 18422 - GATAGGATGGTTAGGGCTTTGCTTCTTGCTGTTTTTCTTTGAAGCTAGTTCATTGTCCTG - 18481
 18482 - CAGGTCCCTTCATCTTCCATACCTAGCCCACTCTTTTAGCCCTTACCTTAAATCTCTCAG - 18541
 18542 - ATAAGTTGGTTTCAAAAGAATGTTAAGTACTGAATCATGTGTGACTGAGACCAGAGATGG - 18601
 18602 - CAAATGAATGGCACACCATTCTCCTTCTCCTGCCCCAGGGCAGGTACCACTGATCTGCA - 18661
 18662 - TCAGAGTTGCCTGCTATTCTCTGGTGTATCCTTCACATCTAGGTGCCCTCAAGCAGCTGT - 18721
 18722 - GTGAGTGTGAGATCTCTGCCATCTCTGGCTGAGATACTGCTGTCTGTGAAGTGTTCCT - 18781
 18782 - CATGACCTTTTTCTTCCCCTTTGAATCCCTCTGTCTGGAGTAGTCCTTGCCTCTTCCCTGC - 18841
 18842 - TCCAGTAGGGCCTTTTCCCTACCCAGCCCCCTGTGCCAGGCTAAGCTGGTACAAGAGCTG - 18901
 18902 - CCAACCTCACAGAGTGTGTTGCTAGGCGAGAGAGGTGCAGGGAAGAGGCAGAGGTATGCAC - 18961
 18962 - CTTCCCCCTTGAAGAGAGGGGAAAGGCTACAGTGGCCCCACATAATTGCCTGACTCACAC - 19021
 19022 - TTCAGCTACCTCTTAATGCCTGTGGAGGAGTGGAGTCTGGATCCCAGTGTGGTGGTG - 19081
 19082 - TAGGAGGCCACAGTGAGCAGGTGGCCCCAGCTGGGTTTCCCAGGTGAGGAATGTGGGGCC - 19141
 19142 - CAGGCAAGGTGCAGCCTTTGCTCACAGCTCCATCCATGTCTAGACCTTCAGGCCAGCTG - 19201
 19202 - CAGATGAGGTTCCCTACCTTTTTCTTCTCTTCTTATTGACCAATCAACCAATCACTACAGC - 19261
 19262 - TGCTCTGCTTCTGCTTTCCAAAGTAGCCAGGTCTGGGCCAGATGCAGGGGAGGTGCCT - 19321
 19322 - ATCCATGAGTGAAGGCCAGTGTCTTCCCTCACCTGGGTGGGTCCCACACTTGTGACCTCAG - 19381
 19382 - TTTTAGGACCAAGATCTGTGTTGGTTTCTTAGATTGCTAGCTTTTCCCTCCAGGGGACCAC - 19441
 19442 - AGCAGGTGAAGCTCAAGAGCGCATGGCTCTGCTAATAGTAAATTGTTTTTCAGGGCCTTGT - 19501
 19502 - CCAGCTGAGAGCTTCATGTCCACCAGATTCTGAGAGGTGTGAGCAGCACTTTTTTTTTTTT - 19561
 19562 - ATTTGTTGTTTGTGTTTTCCATGAGGTTATCGGACCATGGGCTGAGCTCAGGCACCTTCTGT - 19621
 19622 - AGGAGACTGTTATTTCTGTAAAGATGGTTATTTAACCCTTCTCACCCCATCACGGTGGCC - 19681
 19682 - CTGAGGGCTGACCCGGAGGCCAGTGGAGCTGCCTGGTGTCCACGGGGGAGGGCCAAGGCC - 19741
 19742 - TGCTGAGCTGATTCTCCAGCTGCTGCCCCAGCCTTTCCGCCTTGACAGCACAGAGGTGG - 19801
 19802 - TCACCCAGGGACAGCCAGGCACCTGCTCCTCTTGCCCTTCCCTGGGGGAAGGGAGCTGCC - 19861
 19862 - TTCTGTCCCTGTAAGTGTCTTCCCTTATGGCCCAGCCCGGCACTCAGACTTGTGTTGAAGC - 19921
 19922 - TGCACTGGCAGCTTTTTTGTCTCCTTTGGGTATTCAACAGCCAGGGACTTGATTTTGA - 19981
 19982 - TGTATTTTAAACCACATTAAATAAAGAGCTTGTGCTTACTTGTGTTCTCTCCTGACCTG - 20041
 20042 - TGATTCCCTTTGTTTCTGAGTGTGATGCTGTTTCCAGCCCTTCCATCATCACTGACTGTTC - 20101
 20102 - AGGTCTGCTGCAGAGCGCCCATGGTGGTTCCCTGGTATCTTACATATTCCACAGTGTCTT - 20161
 20162 - TGAGCAGTCGCCACAGCCTCAGGATGCTGGCATATTCACTTGAGCTGCCTGAGTGGAGCC - 20221
 20222 - CTTGGCAAAGTTGGCAAGACCCTTGCTCAGAGAGGATCACACACACACAAAAAGTTTT - 20281

Fig. 24 (continued; 9/9)

20282 - CCCTGACCTGGGGGCTCACAGGCTAGTGAAGGGAAAAGGTACTTTTAGCTATAGACAGGT - 20341
 20342 - CAATGGTGTGAGAGCAGAGAGGAGGCCCTGCCCTTCAGCAAGGTGAGGGGGTGATA - 20401
 20402 - CCTGGAATGGCCTTCTGAACCACAGGGCAGGTAGAAGATGAACGTCATTTAGTGATTAAA - 20461
 20462 - TGGTACAGCTGGGAAGCAGGTCCATGGGACTGGGAGAGGGGGTGAGGCTGGGCCCAGAGT - 20521
 20522 - CTGGGTACCAGGTTAAGGAATGTGGGCTAGATCCAGAGGGCAGGGGGGGCAACTGAAGGT - 20581
 20582 - GTTTCATAGGAAATTGATAGGCTCCAGCAGTAAGGCAAAAGGCATGGAGCCAGGCATAG - 20641
 20642 - GCCATTTGAGGCCCAGGTTAAGAGGGGTGGACACTCATCACTGCTATTTGGGTCTGAGCT - 20701
 20702 - GTGGGTAGGCTCCTATAGCCCTGGCCTGCCCAAGGGAATTCACAGGGGCCTCTAATTGTA - 20761
 20762 - TGCATTCCTTAAGGAGAGCACATTCTCTGTTTCAGTTTTTACACCCCCCATTTACCCACCT - 20821
 20822 - CAAGCATGGGACTCCTATATGGGAGACATGCTGCTGGTGGCCTCACCCAGCACCCCTGTTT - 20881
 20882 - TCTCTGGGTCCCTGGGTTGGTCAGGCACAAAGGATGATATGTGCTGAATGCCAGGAAATG - 20941
 20942 - GCAGAGACAACCCACCTGCCCTTCCCTCCAGGCCTCCACAAATAGATGTGCCACAAATGA - 21001
 21002 - CTGTGACAGTCCCAGCAGAGCCTCTGACCCCTCTAGCTGGGTCTGATACATGTTTTCCA - 21061
 21062 - TGCTGGCCATGTTATTTCTAGTCCGAGATCCTCTGGAGGGTGTGGGGGGGGTGCCGCCCT - 21121
 21122 - AACTCTTGGAGATTCCAAGCAAAGCAGCTCTGAGAATAATGAGGTTTCTGACCCCCCAGT - 21181
 21182 - GAAGCAGCTGAGGATGGGAACCAAGGGGTGCTCCCTCTGTGAGCAGCATTACCACTGTC - 21241
 21242 - TACTCTAGCAGCTCCGGTGGGAAGGAGAGGGATTCTGTTGTCCCCAGTCTGGGCCCT - 21301
 21302 - GGTTATTGAAAAAGTTCGGAATTACTCTTTACCCCTGTGGAGTGTCTGAGTGTGGGAAG - 21361
 21362 - TACCCAGGAAGAAGCCCTGAGCAGGTGCCCTCAGGAGCAGTGCCCATGGCTCCCCACATC - 21421
 21422 - AGCCAAGAGGCCCAACCCAGGAAGCCACTCCTGCCCCGGGATGGGGAAGGTGGGCTGGG - 21481
 21482 - TGGCTGTGTGCACTGCCCTGGGCCAGCTCACTTGAGCCTGCTGAGCCGCTGGCCAAACA - 21541
 21542 - TGAGCCTCTCTCCTGTTGTATCAGATGCTGTTCTGGGGACCTGCGCCAGGAGCCTCTGCC - 21601
 21602 - AGGGCTTTAAATAGCTGCCCCATTGATCTGGCTGCAGGCAGCAGCACTCACACTGGGTC - 21661
 21662 - AGCCTCCATCAGGTGCTCAGGTTTCCCTGAGGACTGGAGTCAGGTGCCAGGGAATCGCGT - 21721
 21722 - GGTCTACCTTATGACCTGGTGTCTCCCAACCTGTCTCCTAGGCCTGGGGGGTGGGGAGG - 21781
 21782 - ACTCCTGTCACTTCATCTGCGGCAAAATACAGCCCCCACCCTTACCAGAGAAAAGTGTG - 21841
 21842 - TGGCATTTGTAGAGAGAGGGGTTTGGCCCTCAAAGACTGTTGCTTACTTTTCAGTAGAATG - 21901
 21902 - GGGAATGACACTGGTATCTCCTTAAGGGTTGTTATGGGGATGAAATGTATGTAAAGTGC - 21961
 21962 - TCAATAGGGCACTGGACTCACTCCATTGATGGCTGTCTTTGCTCGAAGTGTCTTCCTGAT - 22021
 22022 - GCTGTGCTGTTGCTGCTTGTGCTTCTTCTGTGCTTACATTCTCTCTCTCACTCACTC - 22081
 22082 - ACTCTGTCTCTCCTCTCCCCCGCCCCACCCCTTTCTGACAAAGCCACCACCATTTTGTA - 22141
 22142 - AGGAACTGTAGCTTCTCTCTGAAACTGCCGGGAAAGGGAAAATCTTTTTAAATAGACAT - 22201
 22202 - CACACAACCAACAGGGTCCCCTAGGTTTCAGGCGGGGAGGTGAGGTGAGTGTAGA - 22255